



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 161522

TO: Elizabeth McElwain
Location: REM-2A11/2C18
Art Unit: 1638
Thursday, April 28, 2005

Case Serial Number: 10/088079

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner McElwain,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC-Biotech/ChemLib

151522

From: McElwain, Elizabeth
Sent: Friday, April 22, 2005 3:50 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Please search 10/088,079 - SEQ ID NO: 1 and 2, and DNA encoding SEQ ID NO: 2
for prior art and for interference.

Thank you,
Beth

Elizabeth F. McElwain, Ph.D.
U.S. Patent and Trademark Office
Tech Center 1600, Art Unit 1638
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571-272-0802
elizabeth.mcelwain@uspto.gov

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4/22/05
1-AA - 01
1-AA - 02P
reverts AA
4/28/05

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 10:53:47 ; Search time 40 Seconds
(without alignments)
815.437 Million cell updates/sec

Title: US-10-088-079-2
Perfect score: 1722
Sequence: 1 MNQRNASMTVIGAGSYGTAL.....AREAAITLGRKRDERSH 339
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1719	99.8	339	2 S47829	glycerol-3-phospha
2	1719	99.8	339	2 G86036	glycerol-3-phospha
3	1719	99.8	339	2 F91189	glycerol-3-phospha
4	1640	95.2	339	2 A80975	glycerol-3-phospha
5	1455	84.5	339	2 A80009	glycerol-3-phospha
6	1242	72.1	344	2 A82050	glycerol-3-phospha
7	1150	66.8	335	2 F64080	glycerol-3-phospha
8	751.5	43.6	346	2 H82637	glycerol-3-phospha
9	703	40.8	332	2 C97111	glycerol-3-phospha
10	672.5	39.1	338	2 AH1316	NAD(P)H-dependent
11	669.5	38.9	338	2 AH1698	NAD(P)H-dependent
12	666.5	38.7	345	2 H69636	glycerol-3-phospha
13	631	36.6	345	2 H83854	NAD(P)H-dependent
14	624.5	36.3	329	2 E81953	glycerol-3-phospha
15	621	36.1	336	2 T35643	glycerol-3-phospha
16	613.5	35.6	341	2 B86792	hypothetical prote
17	608.5	35.3	334	2 C70673	probable gpda2 pro
18	607	35.2	327	2 A12901	glycerol-3-phospha
19	607	35.2	327	2 C97677	probable glycerol-
20	605.5	35.2	338	2 C98109	glycerol-3-phospha
21	604.5	35.1	338	2 E95244	glycerol-3-phospha
22	601.5	34.9	326	2 A13273	glycerol-3-phospha
23	599.5	34.8	332	2 B89926	glycerol-3-phospha
24	575.5	33.4	331	2 E87257	glycerol-3-phospha
25	567	32.9	349	2 T45431	glycerol-3-phospha
26	567	32.9	351	2 A87119	glycerol-3-phospha
27	556	32.3	340	2 H83443	glycerol-3-phospha
28	547	31.8	334	2 A81743	glycerol-3-phospha
29	546	31.7	334	2 G72024	glycerol-3-phospha

30	546	31.7	334	2 E86597	glycerol-3-P dehyd
31	532	30.9	334	2 A71480	probable glycerol-
32	515	29.9	341	2 C70932	probable dehydroge
33	505	29.3	328	2 H75251	glycerol-3-phospha
34	502.5	29.2	313	2 A70441	glycerol-3-phospha
35	482	28.0	330	2 S75139	glycerol-3-phospha
36	460	26.7	354	2 T48649	glycerol-3-phospha
37	448	26.0	307	2 AG2017	glycerol-3-phospha
38	422.5	24.5	433	2 P84832	glycerol-3-phospha
39	415	24.1	356	2 E71252	probable glycerol-
40	403	23.4	312	2 H71876	glycerol-3-phospha
41	403	23.4	312	2 A64640	glycerol-3-phospha
42	381	22.1	298	2 F81325	glycerol-3-phospha
43	366.5	21.3	316	2 A71703	glycerol-3-phospha
44	350	20.3	321	2 E69147	glycerol-3-phospha
45	350	20.3	325	2 G97776	hypothetical prote

ALIGNMENTS

RESULT 1

S47829
glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S47829; B65161
R:Plunkett, G.
submitted to the EMBL Data Library, March 1994
A:Reference number: S47666
A:Accession: S47829
A:Molecule type: DNA
A:Residues: 1-339 <PIU>
A:Cross-references: UNIPROT:P37606; EMBL:U00039; NID:G466582; PIDN:AB18585.1; PID:G1657
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B65161
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-339 <BLAT>
A:Cross-references: GB:AE000439; GB:U00096; NID:G1790036; PIDN:AAC76632.1; PID:G1790037;
C:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: gpaA
C:Superfamily: glycerol-3-phosphate dehydrogenase (NAD)
C:Keywords: oxidoreductase

Query Match	99.8%	Score 1719;	DB 2;	Length 339;
Best Local Similarity	99.7%	Pred. No. 1.2e-118;	Mismatches 0;	Indels 0;
Matches 336;	Conservative 1;			Gaps 0;
Qy	1	MNQRNASMTVIGAGSYGTALAITLARNGHEVLMGHDPHEHATLERDRCNAALPDVPPF	60	
Db	1	MNQRNASMTVIGAGSYGTALAITLARNGHEVLMGHDPHEHATLERDRCNAALPDVPPF	60	
Qy	61	DTLHLESDLATALAASRNILVWPSHVFGVLRQIKPLMRPDARLVWATKGLAETGRLL	120	
Db	61	DTLHLESDLATALAASRNILVWPSHVFGVLRQIKPLMRPDARLVWATKGLAETGRLL	120	
Qy	121	QDVAREALGQIPLAVISGPTFAKELAAGLPTAISLASTDTQTFADDLQQLLHCCKSPRVY	180	
Db	121	QDVAREALGQIPLAVISGPTFAKELAAGLPTAISLASTDTQTFADDLQQLLHCCKSPRVY	180	
Qy	181	SNPDPFVGVLGGAVKKNVIAIGAGSDGIGFCANARTALITRGLAEMSRGLGADPATF	240	
Db	181	SNPDPFVGVLGGAVKKNVIAIGAGSDGIGFCANARTALITRGLAEMSRGLGADPATF	240	
Qy	241	MGWAGLDLVLTCTENOSRRRFGWMLGQGMVQSAOEKIQQVVEGYRNTKEVRELAHRF	300	
Db	241	MGWAGLDLVLTCTENOSRRRFGWMLGQGMVQSAOEKIQQVVEGYRNTKEVRELAHRF	300	

Qy 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339
Db 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339

RESULT 2
G86036
glycerol-3-phosphate dehydrogenase (NAD+) [imported] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G86036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <STO>
A:Cross-references: UNIPROT:P37606; GB:AB005174; NID:G12518358; PIDN:AAG58755.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
C:Superfamily: glycerol-3-phosphate dehydrogenase (NAD)

Query Match 99.8%; Score 1719; DB 2; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.2e-118;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNQNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPHEIATLERDRCNAAFLPDVPPF 60
Db 1 MNQNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPHEIATLERDRCNAAFLPDVPPF 60

Qy 61 DTLHESDLATALAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLAEATGRLL 120
Db 61 DTLHESDLATALAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLAEATGRLL 120

Qy 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDTQTFADDLQQLHCGKSPRVY 180
Db 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDTQTFADDLQQLHCGKSPRVY 180

Qy 181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSRGLGAALGADPATF 240
Db 181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSRGLGAALGADPATF 240

Qy 241 MGMAGLDLVLTCTENOSRNRFFGMMLGQGMVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
Db 241 MGMAGLDLVLTCTENOSRNRFFGMMLGQGMVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339
Db 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339

RESULT 4
AB0975
glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) - Salmonella enterica subsp. enter.
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
C:Accession: AB0975
R:Parkhill, J.; Dougan, K.D.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0975
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03294.1; PID:G16504915; GSPDB:GN00176
C:Genetics:
C:Superfamily: glycerol-3-phosphate dehydrogenase (NAD)
C:Keywords: oxidoreductase

Query Match 95.2%; Score 1640; DB 2; Length 339;
Best Local Similarity 94.7%; Pred. No. 7.3e-113;
Matches 321; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNQNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPHEIATLERDRCNAAFLPDVPPF 60
Db 1 MNQNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPHEIATLERDRCNAAFLPDVPPF 60

Qy 61 DTLHESDLATALAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLAEATGRLL 120
Db 61 DTLHESDLATALAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLAEATGRLL 120

Qy 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDTQTFADDLQQLHCGKSPRVY 180
Db 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDTQTFADDLQQLHCGKSPRVY 180

Qy 181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSRGLGAALGADPATF 240
Db 181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSRGLGAALGADPATF 240

Qy 241 MGMAGLDLVLTCTENOSRNRFFGMMLGQGMVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
Db 241 MGMAGLDLVLTCTENOSRNRFFGMMLGQGMVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339
Db 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339

RESULT 3
F91189
glycerol-3-phosphate dehydrogenase (NAD+) [imported] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C:Accession: F91189
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91189
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <HAY>
A:Cross-references: UNIPROT:P37606; GB:BA000007; PIDN:BA37909.1; PID:G13363961; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952

Query Match	84.58;	Score 1455;	DB 2;	Length 339;
Best Local Similarity	84.24;	Pred. No. 2.7e-99;		
Matches 283;	Conservative 24;	Mismatches 29;	Indels 0;	Gaps 0;
Qy 1	MMORNASMTVIGAGSYGTALAIATLARNGHVVVLWGHDPHEHATLERDRCNAAFLDPVPP	60		
Db 1	MMTNPSMAVIGAGSYGTALAIATLARNGHVVVLWGHDPKHQQLOQDRCNRAFLDPAFP	60		
Qy 61	DTLHLESDLATALAASRNILVWPSHVFGVLRQIKPLMRPDPARLVWATKGLEAETGRLL	120		
Db 61	DTLRLLETDLACALAASRDVLVWPSHVFGVLRHQLKPHLRKDARLVWATKGLEAETGRLL	120		
Qy 121	QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQOLLLHCGKSFVY	180		
Db 121	QDVAREVLGEAIPAVISGPTFAKELAAGLPTAIALASTDQFSEDQLQOLLLHCGKSFVY	180		
Qy 181	SNPDFTGVQLGGVAKNVIAITGAGMSDGI GFGANARTALITRGLAEMSRIGALGADPATF	240		
Db 181	SNPDFTGVQLGGVAKNVIAITGAGMSDGI GFGANARTALITRGLAEMTRIGTALGADPSTF	240		
Qy 241	MGMAGLGDVLVTCTENOSRNRFCFQMLGCGQMDVQSAQEKIQGVVEGYRNTKEVRELAHRF	300		
Db 241	MGMAGLGDVLVTCTDQNSRNRFCGIMLGQGLGVKEAQDNIQGVVEGYRNTKEVRLAQEH	300		
Qy 301	GVEMPTTEBIYQVLYCGKNAREAAATLLGRARKDER	336		
Db 301	GVEMPTTEQIQVLYCHKNAREAAATLLGRYKQDEK	336		

RESULT 6

A82050
glycerol-3-phosphate dehydrogenase (NAD+) VC2651 [imported] - Vibrio cholerae (strain N1)
C.Species: Vibrio cholerae
C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Aug-2004
C.Accession: A82050
R.Heldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Harrison, D.; Esmolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1. R.R.D.: Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

	Query Match	66.8%	Score 1150;	DB 2;	Length 335;
	Best Local Similarity	67.4%;	Pred. No. 6e-77;		
	Matches 221; Conservative	48;	Mismatches 59;	Indels 0;	Gaps 0;
Qy	8 MTVIGAGSYCTALAITLARNGHEVVWLGMDPEHIATLERDRCNAAFLPVPFDDTLHLES	67			
	: :: :	:	:	:	:
Dd	8 ITVLGAGSYCTALAITFRSGNSPTHLWGHNPAIIAQMTQRQNYRFLPDVIPFDLHLES	67			
Ov	68 DLATAAASNNILVWPSPHFVEGLROIKPLMRPDLRWATKGLEAETGRLLDVAEA	127			

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Db      68  NLQAAMEYSQDILTVPSHAFGETLIKIKPHLKAHHLRIWATKGLERNTGRLLQTVVEEQ 127
QY      128  LGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDDQLLHCCKSPRVYSNPDPFIG 187
Db      128  LGTQYPLAVISGPTFAKELAAQLPSAITLAANNEQFAREFQSRIHCSKGRFVINSMTG 187
QY      188  VOLGGAVKNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLGAALGADPATFMGMAGLG 247
Db      188  VOLGGAIKWVIAIGAGISDGMGFCANARTALITRGLAEMSRGLGAALGADPATFMGMAGLG 247
QY      248  DLVLTCTENOSRNRFFGMMLGQGMVQSAOEKIQGVVEGYRNTKEVRELAAHRRGVEMPIIT 307
Db      248  DLVLTCTDNOSRNRFFGLMKGKGLDAQMAMENIQGVVEGYRNTKEAYLLAQROGVEMPIIT 307
QY      308  EEIYQVLYCGKNAREAAALTLIGRARKDE 335
Db      308  EEIYQVLYCGKNAREAAALTLIGRACKGE 335

RESULT 8
glycerol-3-phosphate dehydrogenase XF1802 [imported] - Xylella fastidiosa (strain 955c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: H82637
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: H82637
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-346 <STM>
A/Cross-references: UNIPROT:Q9PCH7; GB:AE004001; GB:AE003849; NID:G9106864; PIDN:AAF8461
A/Experimental source: strain 955c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorfi, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XF1802
C/Superfamily: glycerol-3-phosphate dehydrogenase (NAD)

Query Match 43.6%; Score 751.5; DB 2; Length 346;
Best Local Similarity 46.7%; Pred. No. 1e-47;
Matches 156; Conservative 54; Mismatches 111; Indels 13; Gaps 3;

QY      8  MTVIGAGSYGTALAITLARGHEVVLWGHDPHEIATLERDRCNAAFLPDVFPFDTLHLES 67
Db      8  IAVLGAGSWGTAALVARIHAIPTILMGDRGVGIQSIDIQRNPRYLPSPMLPOTLRATT 67

QY      68  DLATALAASRNILVVPVSHVGEVLRQIKPLMRDPARLVWATKGLAEATGRLLQDVAREA 127
Db      68  DLAAAVSGADWLVAVPSYAFETTLRLAPLLSTGVGVAMATKGFEPGSGRFLHEVAREI 127

QY      128  LGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDDQLLHCCKSPRVYSNPDPFIG 187
Db      128  LGGDAPLAVVTGSPFAKEVTLGLPTAVTVHGEYARPTQMVANAMH-GPMFRAYTGNVDIG 186

QY      188  VOLGGAVKNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLGAALGADPATFMGMAGLG 247
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Db      187  AEIIGGAMKNVLAIVAIGADGMQLGMNARAGLIITRGLNEMRLSVAIGARPETLMGLAGLG 246
QY      248  DLVLTCTENOSRNRFFGMMLGQGMVQSAOEKIQGVVEGYRNTKEVRELAAHRRGVEMPIIT 307
Db      247  DLVLTCTGDLRNRRLGFGALGSGSLDAIREIGQVVESVQTSDEVMRQAQEHGVLEPIS 306
QY      308  EEIYQVLYCGKNAREAAALTLIGRARKDE 335
Db      307  EAVRAVLREBITPYAGMKA-----LLAREQKPE 334

RESULT 9
glycerol-3-phosphate dehydrogenase [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 16-Aug-2004
C/Accession: C97111
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: C97111
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-332 <KUR>
A/Cross-references: UNIPROT:Q97ID6; GB:AE001437; PIDN:AAK79678.1; PID:gl5024677; GSPDB:G
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC1712
C/Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)

Query Match 40.8%; Score 703; DB 2; Length 332;
Best Local Similarity 42.1%; Pred. No. 3.5e-44;
Matches 138; Conservative 71; Mismatches 117; Indels 2; Gaps 2;

QY      8  MTVIGAGSYGTALAITLARGHEVVLWGHDPHEIATLERDRCNAAFLPDVFPFDTLHLES 67
Db      4  VTFIGGSGFTALAIMLAKKHNVVWDRNKEILEIDINTLRTNTRYLPNNIIPCCKVAVD 63
QY      68  DLATALAASRNILVVPVSHVGEVLRQIKPLMRDPARLVWATKGLAEATGRLLQDVAREA 127
Db      64  DIEKAATESKIVLVAVPSFAIREVCVKIGFLAEQDIIISIAKMEBETKRLSEVVKEE 123
QY      128  LGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDDQLLHCCKSPRVYSNPDPFIG 187
Db      124  LYKN-PVVVLGSGSHAEVANDIPTTVVVTSTDMKYAEVQDVF-MTNSFRVYTNDSIVG 181
QY      188  VOLGGAVKNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLGAALGADPATFMGMAGLG 247
Db      182  VEIIGGAVKNIIALASGIDGIDGYDNTKAAIMTRGMSSEIMRIGVKLGKGKDETFPGLTGMG 241
QY      248  DLVLTCTENOSRNRFFGMMLGQGMVQSAOEKIQGVVEGYRNTKEVRELAAHRRGVEMPIIT 307
Db      242  DLIVTCTSMHSRNRKAGILIGRGSCREACDKIGWVEGVKACHTFVELKESLGVSMPIIT 301
QY      308  EEIYQVLYCGKNAREAAALTLIGRARKDE 335
Db      302  TSLYKVLFFENGDPKKEVYELMARDKKNE 329

RESULT 10
AH1316
NAD(P)H-dependent glycerol-3-phosphate dehydrogenase homolog gpaA [imported] - Listeria
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C/Accession: AH1316
R/Glasser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
```


Db	184	VVGCELGGA	VKNVIGLAVGIADGMGLGDNAGSLITRGLAETTRGLGVALGADPLTFSGLA	243
Qy	245	GLGDLVLTCTENQSRNR	RRFGWMLGOGMDVQSAQEKIGOVVEGYRNTKEVRELAHFGVEM	304
Db	244	GLGDLVATCSSL	SRNHTFTGTLGKGMTLEETNAVTKOTAEGVKSCSVLDLARRHGVD	303
Qy	305	PITEEYOVLYCGKNAREAA	LTLLGRARKDER	336
Db	304	PITETVAIVH	BGKSPVAVKELMSRSAPKPER	335

Search completed: April 27, 2005, 11:03:28
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2005, 13:52:02 ; Search time 652 Seconds

(without alignments)
3077.902 Million cell updates/sec

Title: US-10-088-079-2

Perfect score: 1722

Sequence: 1 MNQRNASMTVIGAGSYGTAL.....AREALTLGRKDERSSH 339

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgm2_1/USPTO.spool/US10088079/runat_27042005.101459.11238/app_query.fasta_1.519
-DB=N_Geneseq_16Dec04 -QMT=fascap -SUFFIX=ring -MINMATCH=0.1 -LOOFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blotum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10088079 @CGN 1.1.644 @runat_27042005.101459.11238 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=1120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq_16Dec04:.*
1: Geneseq_1980s:.*
2: Geneseq_1990s:.*
3: Geneseq_2000s:.*
4: Geneseq_2001as:.*
5: Geneseq_2001bs:.*
6: Geneseq_2002as:.*
7: Geneseq_2002bs:.*
8: Geneseq_2003as:.*
9: Geneseq_2003bs:.*
10: Geneseq_2003cs:.*
11: Geneseq_2003ds:.*
12: Geneseq_2004as:.*
13: Geneseq_2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1722	100.0	1020	5	Aaf57428 E. coli g
2	1719	99.8	1020	4	Aas52655 E. coli D
3	1719	99.8	1020	8	ACA32689 Prokaryot
4	1719	99.8	1020	13	Adt48853 Bacterial
5	1640	95.2	1020	8	ACA51335 Prokaryot

6	1635	94.9	1017	8	ACA31966	ACA31966 Prokaryot
7	1587	92.2	1017	8	ACA35838	ACA35838 Prokaryot
8	1587	92.2	1038	11	ACH97774	ACH97774 Klebsiell
9	1556	90.4	1023	8	ACA49224	ACA49224 Prokaryot
10	1455	84.5	1020	8	ACA54019	ACA54019 Prokaryot
11	1420	82.5	1023	10	ADF03046	ADF03046 Bacterial
12	1411	81.9	1011	8	ACA44463	ACA44463 Prokaryot
13	1393.5	80.9	1023	10	ACF70491	ACF70491 Photorhab
14	1393.5	80.9	69727	10	ACF65374	ACF65374 Photorhab
15	1393.5	80.9	110000	10	ACF67367_35	Continuation (36 o
16	1373	79.7	990	13	ADS45613	ADS45613 Bacterial
17	1372	79.7	990	13	ADT46572	ADT46572 Bacterial
18	1242	72.1	1035	8	ACA53490	ACA53490 Prokaryot
19	1192	69.2	1014	8	ACA43241	ACA43241 Prokaryot
20	1154	67.0	135356	13	ADT05646	Adt05646 Haemophil
21	1150	66.8	1008	4	AAS53331	Aas53331 Haemophil
22	1150	66.8	1008	8	ACA34182	ACA34182 Prokaryot
23	1150	66.8	110000	2	AAT42063_06	Continuation (7 of
c 24	1141	66.3	4711	13	ADT05428	Adt05428 Haemophil
c 25	864	50.2	781	6	ABQ21987	Abq21987 Oligonuc
26	864	50.2	781	6	ABQ21986	Abq21986 Oligonuc
27	827	48.0	781	6	ABQ21989	Abq21989 Oligonuc
c 28	827	48.0	781	6	ABQ21988	Abq21988 Oligonuc
29	806	46.8	987	8	ACA37060	ACA37060 Prokaryot
30	794.5	46.1	1002	13	ADT41591	Adt41591 Bacterial
31	794.5	46.1	1002	13	ADS63997	Ads63997 Bacterial
32	794.5	46.1	1020	13	ADS63622	Ads63622 Bacterial
33	751.5	43.6	1041	13	ADT42864	Adt42864 Bacterial
34	738.5	42.9	1002	13	ADS57169	Ads57169 Bacterial
35	720.5	41.8	1002	13	ADT41768	Adt41768 Bacterial
36	709.5	41.2	1020	8	ACA21995	ACA21995 Prokaryot
37	703	40.8	999	8	ACA27525	ACA27525 Prokaryot
38	694	40.3	1029	8	ACA29483	ACA29483 Prokaryot
39	692	40.2	1065	8	ACA33900	ACA33900 Prokaryot
40	692	40.2	1071	10	ADC30723	Adc30723 E. faeciu
41	681	39.5	1062	10	ADC91772	Adc91772 E. faeciu
42	677.5	39.3	1032	9	ADB08817	Adb08817 Alloiooc
43	677.5	39.3	1032	9	ADB08815	Adb08815 Alloiooc
44	677.5	39.3	1032	9	ADB08819	Adb08819 Alloiooc
45	677.5	39.3	110000	9	ADB12064_07	Continuation (8 of

ALIGNMENTS

RESULT 1
AAF57428
ID AAF57428 standard; DNA; 1020 BP.
XX
AC AAF57428;
XX
DT 11-JUN-2001 (first entry)
XX
DE E. coli gpsA2FR encoding DNA.
XX
KW Glycerol-3-phosphate dehydrogenase; G3PD; feedback inhibition; oil seed;
KW genetic transformation; fatty acid; glycerolipid; osmotic stress; gpsA;
KW gpsA2FR; allele; ds.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
CDS 1..1020
FT /*tag= a
FT /product= "gpsA2FR"
FT mutation 765
FT /*tag= b
FT /note= "there is a point mutation at this position as
FT compared to the wild-type gpsA gene, which makes the gene
FT feed-defective; wild-type GAC codon is changed to GAA
FT codon"
XX
XX WO200121820-A1.
XX

PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-CA001096.
 XX
 PR 22-SEP-1999; 99US-0155133P.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Zou J, Wei Y, Periappuram C, Selvaraj G, Datla R;
 XX
 DR WPI: 2001-257996/26.
 DR P-PSDB; AAB62189.
 XX
 PR Manipulating glycerol-3-phosphate metabolism of plant for enhancing
 PT stress tolerance, altering fatty acid content in glycerolipids, by
 PT expressing in plant feedback defective glycerol-3-phosphate dehydrogenase
 PT gene.
 XX
 PS Claim 5; Fig 1; 39pp; English.
 XX
 CC The invention provides a method for genetically transforming a plant so
 CC that it expresses a heterologous glycerol-3-phosphate dehydrogenase
 CC (G3PD) that is less sensitive to feedback inhibition than wild-type G3PD.
 CC The method involves providing a vector comprising a DNA sequence encoding
 CC G3PD that is less sensitive to feedback inhibition than wild-type G3PD
 CC and transforming the plant with the vector. The method is useful for
 CC expressing a heterologous G3PD less sensitive to feedback inhibition than
 CC wild-type G3PD in an oil seed bearing plant, such as Arabidopsis thaliana
 CC or Brassica. The vectors are useful for producing a genetically altered
 CC plant having altered fatty acid content in its glycerolipids, especially
 CC elevated levels of C16 fatty acids and increased osmotic stress tolerance
 CC relative to the wild type. The present sequence represents the DNA
 CC encoding the E. coli gpaA2FR protein. The gene gpaA2FR is an allele of
 CC the E. coli gpaA gene, and encodes an altered version of the GPDH protein
 CC defective in feedback inhibition. This gpaA2FR gene can be used in the
 CC vectors and method of the invention
 XX
 SQ Sequence 1020 BP; 214 A; 274 C; 304 G; 228 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,46e-158 Length: 1020
 Score: 1722.00 Matches: 339
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-10-088-079-2 (1-339) x AAF57428 (1-1020)

Qy	1	MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu	20
Db	1	ATGAACCAACGTAATGCTCAATGACTGTGATCGTGGCGCTCGTACGGCACGCTCTT	60
Qy	21	AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis	40
Db	61	GCCATACCTCGGCAAGAAATGGCCAGAGTTGTCTCTGGGGCCATGACCCCTGAACAT	120
Qy	41	IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro	60
Db	121	ATGCAACGCTTGAACGCGACCGCTGTAAACGCGCTTCTCCCGATGTGCTTTTCCC	180
Qy	61	AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaSerArgAsnIleLeu	80
Db	181	GATACGCTCCATCTTGAAGAGGATCTCGCCACTCGCTGGCAGCCGCGTAATATTCTC	240
Qy	81	ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg	100
Db	241	GTCTGTGTACCCACCATGCTTTTGGTGAAGTGTCTGGCCAGATTAACCACTGATGCGT	300
Qy	101	ProAspAlaArgLeuValTrpAlaThrIysGlyLeuGluAlaGluThrGlyArgLeuLeu	120
Db	301	CCTGATGCGCTGTGTGTGGCGCACCAAGGGCTGGGAAGCGGAACCGGACGCTCTGTTA	360

Qy	121	GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro	140
Db	361	CAGGACGTGGCGGTAGGGCTTTAGGCGATCAAAATTCGCTGGCGTATCTCTGGGCCCA	420
Qy	141	ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp	160
Db	421	ACGTTTGGAAAGAACCTGGCGGAGGTTTACCGACAGCTATTTCGCTGGCTCGACCGAT	480
Qy	161	GlnThrPheAlaAspAspLeuGlnLeuLeuHisCysGlyLysSerPheArgValTyr	180
Db	481	CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGGCGCAAAAGTTTCCGCGTTTAC	540
Qy	181	SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle	200
Db	541	AGCAATCCGATTTTCATTGGCTGCGAGCTTGGCGGCGCGTGAATAACGTTATTGCCATT	600
Qy	201	GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr	220
Db	601	GGTGGGGGATGTCGACGCGTATCGGTTTGGTGGGATGCGGTACGCGCGCTGATCACC	660
Qy	221	ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe	240
Db	661	CGTGGGCTGGCTGAAATGTGCGCTTGTGTGGCGGCTGGCTGGCACCTGCTT	720
Qy	241	MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn	260
Db	721	ATGGCGATGGCGGGCTTGGCGATCTGGTCTTACCTGTACCGAATAACCGTCCGTAAC	780
Qy	261	ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle	280
Db	781	CGCGTTTGGCATGATGCTCGGTGAGGCGATGGAATGACAAAGCGCGCAGGAGAGATT	840
Qy	281	GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe	300
Db	841	GGTCAGGTGTGGAAAGGCTACCGCAATACGAAAGAGTCCGCAACTGGCGCATCGCTTC	900
Qy	301	GlyValGluMetProIleThrGluIleTyrGlnValLeuTyrCysGlyLysAsnAla	320
Db	901	GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATTTCGCGAATAACGCG	960
Qy	321	ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis	339
Db	961	CGCGAGCGCAGCATTTACTTACTAGTCTGTCAGCGAAGCGCGCAGCGCAGCGCAC	1017
RESULT 2			
ID	AAS52655		
XX	AAS52655 standard; DNA; 1020 BP.		
AC	AAS52655;		
XX			
DT	13-FEB-2002 (first entry)		
XX			
DE	E. coli DNA for cellular proliferation protein #377.		
XX			
KW	Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;		
KW	antibacterial; drug design.		
XX			
OS	Escherichia coli.		
XX			
PN	WO200170955-A2.		
XX			
PD	27-SEP-2001.		
XX			
PF	21-MAR-2001; 2001WO-US0009180.		
XX			
PR	21-MAR-2000; 2000US-0191078P.		
PR	23-MAY-2000; 2000US-0206848P.		
PR	26-MAY-2000; 2000US-0207272P.		
PR	23-OCT-2000; 2000US-0242578P.		
PR	27-NOV-2000; 2000US-0253625P.		
PR	22-DEC-2000; 2000US-0257931P.		
PR	16-FEB-2001; 2001US-0269308P.		
XX			

(ELIT-) ELITRA PHARM INC.

Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
Yamamoto RT, Xu HH;
WPI; 2001-611495/70.
P-PSDB; AAU34796.

New polynucleotides for the identification and development of
antibiotics, comprise sequences of antisense nucleic acids.

Claim 27; SEQ ID NO 6292; 511bp; English.

The invention relates to antisense inhibitors of genes essential to
prokaryotic cellular proliferation, their use in identifying the genes,
their use in the discovery of novel antibiotics, the essential genes,
themselves and the encoded proteins. The prokaryotes used are *Escherichia*
coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
Pseudomonas aeruginosa and *Enterococcus faecalis*. The invention is also
useful for the identification of potential new targets for antibiotic
development. The antisense nucleic acids can also be used to identify
proteins used in proliferation, to express these proteins, and to obtain
antibodies capable of binding to the expressed proteins. The proteins can
be used to screen compounds in rational drug discovery programmes. The
antisense nucleic acid sequence is also useful to screen for homologous
nucleic acids which are required for cell proliferation in a wide variety
of organisms. The present sequence encodes an essential prokaryotic
cellular proliferation protein. Note: The sequence data for this patent
did not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6,786-158 Length: 1020
Score: 1719.00 Matches: 338
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.71% Mismatches: 0
Query Match: 99.83% Indels: 0
DB: 4 Gaps: 0

US-10-088-079-2 (1-339) x AAS52655 (1-1020)

1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGGCGCTGTACGGACCCGCTCTT 60
21 AlalThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
61 GCCATCACCTGGCAAGAAATGGCCACGAGGTGTCTCTGGGGCCATGACCTGAACAT 120
41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
121 ATCGCAACGCTTGAACGCGACCGCTGTAAACGCGCGTTTCTCCCGATGTGCTTTCC 180
61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
181 GATACGCTCCATCTTGAAGAGGATCTGCCACTGCGCTGGACGCGCGTAATATCTC 240
81 ValValValProSerHisValPheGlyGluValValLeuArgGlnIleLysProLeuMetArg 100
241 GTCGTGCTACCCAGCCATGCTTTTGGTGAAGTGTCTGGCCAGATTAAACCACTGATGCGT 300
101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
301 CCTGATGCGCGTCTGGTGGCGCACCAAGAGGCTGGAAAGGCGTGAACCGGACGCTGTTA 360
121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
361 CAGGACGTGGCGCGTGGAGCCCTTAGCGGATCAATTCGCTGGCGGTATCTCTGGCCCA 420
141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160

Db 421 ACGTTTGGAAAGAACTGGCGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
Qy 161 GlnThrPheAlaAspAspLeuGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
Db 481 CAGACCTTTTGGCGATGATCTCCAGCAGCTGTGCACTCGCGCAAAAGTTTTCGCGTTTAC 540
Qy 181 SerAsnProAspPheIleGlyValLeuLeuGlyAlaValLysAsnValIleAlaIle 200
Db 541 AGCAATCCGATTTTCATTTGGCGTGCAGCTTGGCGGCGGTGMAAAACGTTATTGCCATT 600
Qy 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
Db 601 GGTGGCGGATGTCCGACGTTATCGGTTTGGTGCAGATGGCGGTACGCGCTGATCACC 660
Qy 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
Db 661 CGTGGCTGGCTGAAATGTCCGCTTCTGGTGGCGGTGGGTGGCGACCCCTGCCACCTTT 720
Qy 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
Db 721 ATGGGCATGGCGGGCTTGGCGATCTGGTGTACCTGTACCGACACCAACGATCGCGTAAC 780
Qy 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
Db 781 CGCGCTTTTGGCATGATGCTCGTCAGGCGCATGGATGTACAAAGCGCGCAGAGAAGATT 840
Qy 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
Db 841 GGTGAGTGGTGGAAAGGCTACCGCAATACGAAAGAAAGTCCGCAACTGGCGCATCGCTTC 900
Qy 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
Db 901 GCGCTTGAATGCCAATACCGAGGAATTTATCAAGTATTATATTGCGGAAAAAAGCGG 960
Qy 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
Db 961 CGCGAGGCGAGCATTTGACTTTACTAGTCTGTGCGCAAGAGGACGAGCGCAGCGACCCAC 1017
RESULT 3
ID ACA32689 standard; DNA; 1020 BP.
XX ACA32689;
AC ACA32689;
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #14346.
DE Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Escherichia coli.
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR P-PSDB; ABU28819.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX
 PS Claim 14; SEQ ID NO 20559; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence data is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6 78e-158 Length: 1020
 Score: 1719.00 Matches: 338
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.71% Mismatches: 0
 Query Match: 99.83% Indels: 0
 DB: 8 Gaps: 0

US-10-088-079-2 (1-339) x ACA32689 (1-1020)

Qy 1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
 Db 1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGTGGCGGCTCGTACGGCACCGCTCTT 60
 Qy 21 AlalleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
 Db 61 GCCATCACCCCTGGCAAGAAATGGCCACGAGGTGTCTCTCGGGCCATGACCCCTGAACAT 120
 Qy 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
 Db 121 ATCGCAACGCTTGAAACGGACCGCTGTACCGCGGTTCTCCCGATGTGCCCTTTCC 180
 Qy 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
 Db 181 GATACGCTCCATCTTGAAGCGATCTGCCACTCGCTGGCAGCGCGTAATATTCTC 240
 Qy 81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
 Db 241 GTGCGTGACCGACCGATGCTTTGGTGAAGTGTGGCCAGATTAACCACTGATCGGT 300
 Qy 101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120

Db 301 CCTGATCGCGCTCTGGTGTGGCGCACCAAGGGCTGGAAGCGGNAACCGGACGCTCTGTTA 360
 Qy 121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
 Db 361 CAGGACGTGGCGCTGAGGCTTAGCGGATCAAAATTCGCTGGCGGTATCTCTGGGCCA 420
 Qy 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
 Db 421 ACGTTTCGAAAGAACATGGCGGCGAGGTATACCGACAGCTATTTCCGTGGGCTCGACCGAT 480
 Qy 161 GlnThrPheAlaAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
 Db 481 CAGACCTTTCCCGATGATCTCCAGCAGCTGTCACACTGGCGCAAAAGTTTCCGCGTTAC 540
 Qy 181 SerAsnProAspPheIleGlyValGlnLeuGlyAlaValLysAsnValIleAlaIle 200
 Db 541 AGCAATCCGATTTTCATTTGGCTGCGAGCTTGGCGGCGCGTGAATAACGTTATTGCCATT 600
 Qy 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
 Db 601 GGTGCGGGGATGTCGACGATATCGGTTTGGTGGCAATGCGGTCAGCGGCTGATCACC 660
 Qy 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
 Db 661 CGTGGGCTGGCTGAAATGTCGGTCTTGGTGGCGGCTGGGTGCCGACCTGCCACCTTT 720
 Qy 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
 Db 721 ATGGGCAATGGCGGCTTGGCATCTGGTCTTGGTGGCGGCTGGGTGCCGACCTGCCACCTTT 780
 Qy 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluValIle 280
 Db 781 CGCGCTTTTGGCATGATGTCGGTTCGGTTCGGGCTGGGTGCCGACCGGAGGAAGATT 840
 Qy 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
 Db 841 GGTCAAGTGTGGAGGCTACCGCAATACGAAGAGTCCGCGAAGTCCGCGACTCGCTTC 900
 Qy 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
 Db 901 GGGCTTGAATGCAATAACCGAGGAAATTTATCAAGTATTATATTCGGGAAAAACGCG 960
 Qy 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
 Db 961 CGCGAGGACGATTTGACTTACTAGGTGTCGACGCAAGGACGAGCGCAGCGACCGAC 1017
 RESULT 4
 ID ADT48853
 ID ADT48853 standard; cDNA; 1020 BP.
 XX AC ADT48853;
 XX DT
 XX 02-DEC-2004 (first entry)
 XX DE Bacterial polynucleotide #23604.
 XX KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polynucleotide; gene; ss.
 XX OS Bacteria.
 XX PN US2003233675-A1.
 XX PD 18-DEC-2003.
 XX PF 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 XX (GOLD/) GOLDMAN B S.
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 47291; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: Length: 1020
 Score: 1719.00 Matches: 338
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.71% Mismatches: 0
 Query Match: 99.83% Indels: 0
 DB: 13 Gaps: 0

US-10-088-079-2 (1-339) x AD748953 (1-1020)

QY 1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
 DB 1 ATGAACCAACGTAATGCTTCATGACTGTGATCGGTGGCGCTCGTACGCCACCGCTCTT 60
 QY 21 AlalleThrLeuAlaArgAsnGlyHisGluValValLeuTyrGlyHisAspProGluHis 40
 DB 61 GCCATCACCCCTGGCAAGAAATGCCACGAGGTGTCTCTGGGGCCATGACCCCTGAACAT 120
 QY 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
 DB 121 ATCGGAACGCTTGAACGCCGACCGCTGTAAACGCCGGGTTCCTCCCGATGTGCTTTCC 180
 QY 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
 DB 181 GATACGCTCACTTGAAGCGATCTCGCCACTGCGCTGGCAGCCGCGGTAATATCTC 240
 QY 81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleGlyProLeuMetArg 100
 DB 241 GTTCGTGTAACCCAGCCATGCTCTTTGTTGAAGTGTCTGCGCCAGATTAAACCACTGATGG 300

QY 101 ProAspAlaArgLeuValTrrAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
 DB 301 CCTGATGGCGCTCTGGTGTGGCGCACCAAGAGGGCTGGAGAGCGGAACCGGACGCTGTGTTA 360
 QY 121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
 DB 361 CAGGACGTGGCGCTGAGGCCCTTAGCGCATCAAAATTCGCTGGCGGTATCTCTGGCCCA 420
 QY 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
 DB 421 ACGTTTCGGAAGAACCTGGCGCGAGGTTCACGACAGCTATTTTCGCTGGCTCGACCCGAT 480
 QY 161 GlnThrPheAlaAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
 DB 481 CAGACCTTTGCGGATGATCTCCAGCAGCTGTCACCTGCGGCNAAGTTTCGCGTTTAC 540
 QY 181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaLe 200
 DB 541 AGCAATCCGATTTTCATTTGGCGTGCAGCTTGGCGCGCGGTGMAAAACGTTATTGCCATT 600
 QY 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
 DB 601 GGTGCGGGGATGTCGACGGTATCGGTTCGTAATGCGCGTACGCGCTGATCACC 660
 QY 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
 DB 661 CGTGGCTGGCTGAAATGTTCGCTCTTGGTGGCGGCTGGGTGGCGACCTGCCACCTTT 720
 QY 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
 DB 721 ATGGGCATGGCGGCGCTTGGCGATCTGGTGTCTTACCTGACCGAACACAGTCGCGTAAC 780
 QY 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnLysIle 280
 DB 781 CGCCGTTTGGCATGATGCTCGGTGAGGCGATGATGTACAAAGCGCGCAGAGAGATT 840
 QY 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
 DB 841 GGTCAAGTGGTGGAGGCTACCGCAATACGAAAGATCCCGGAACTCGCGCATCGCTTC 900
 QY 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
 DB 901 GCGGTTGAAATGCCAATAACCGAGAAATTTATCAAGTATTATATTTGCGGAAAAAACGCG 960
 QY 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
 DB 961 CGCAGGCGAGCATTTGACTTTTACTAGTGTGTCACGCAAGGACGAGCGCAGAGCCAC 1017

RESULT 5
 ACAS1335
 ID ACAS1335 standard; DNA; 1020 BP.
 XX ACAS1335;
 AC ACAS1335;
 DT 19-JUN-2003 (first entry)
 XX
 DE Prokaryotic essential gene #32992.
 XX
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX
 OS Salmomella typhi.
 XX
 PN WO200277183-A2.
 XX
 XX 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX P-PSDB; ABU47465.
 DR WPI; 2003-029926/02.
 DR P-PSDB; ABU47465.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 39205; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1020 BP; 217 A; 271 C; 316 G; 216 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,41e-150 Length: 1020
 Score: 1640.00 Matches: 321
 Percent Similarity: 97.05% Conservative: 8
 Best Local Similarity: 94.63% Mismatches: 10
 Query Match: 95.24% Indels: 0
 DB: 8 Gaps: 0

US-10-088-079-2 (1-339) x ACA51335 (1-1020)

Qy 1 MetAenGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
 Db 1 ATGAACCAAGTAATGCGTCAATGACATCGTGGCGGCTCGTACGGCACCAGCTCTC 60
 Qy 21 AlarLeThrLeuAlaArgAsnGlyHisGluValValLeuTyrGlyHisAspProGluHis 40
 Db 61 GCCATCATCTTGGCGAGAAACGGCCACCAGGTTGTCTTGTGGGGCCACGCCAAACAT 120
 Qy 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
 Db 121 ATCGCGACCTTGGAGCAGCATCGTGTCAACGTCGCGGTTCCCTCCCGATGTGCTTTTCCC 180

Qy 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
 Db 181 GATACGTTTACCTTGGAAAGCGACTTAGCAACCGCGCTGGCGGCAGCTCGTAACATCTG 240
 Qy 81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
 Db 241 GTGGTGTGTGCACGCCATGTTTTCAGCGACGTGCTGGCGCAGATTAAACCGCTGATGCGT 300
 Qy 101 ProAspAlaArgLeuValTyrAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
 Db 301 CCGGATCGCGTCTGGTATGGCGGACCAAGGCGCTGGAAGCGGAAACGGGCGCTGTTG 360
 Qy 121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
 Db 361 CAGGATGTCGCTCGCGAGGCGTTAGGCGCATCAATCCGCTGGCGGTGATTTCCGGTCCG 420
 Qy 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
 Db 421 ACCTTCGCTAAGAGCTGGCGGGGGTTCGCGACGCGCATCTCGTAGCTCAACCGAT 480
 Qy 161 GlnThrPheAlaAspAspLeuGlnGlnLeuHisCysGlyLysSerPheArgValTyr 180
 Db 481 GAGACCTTTGCGGACGATCTCCAGCAACTGTTGCACCTGCGGAAAAAGTTTTTCGGCTAT 540
 Qy 181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
 Db 541 ATCAATCCGATTTTATTCGCGGTGCAGCTTGGCGGGCGGTGAAAAACGTTGCGGAT 600
 Qy 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
 Db 601 GCGCGGGGATGTCTGACGCGATCGGCTTGGCGGGAACGCCCGCACGGGCTAATCACG 660
 Qy 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
 Db 661 CGTGGACTGACCGAAATGTCCGCGCTTGGCGGACGCTTGGTGGCGATCCCGCCACCTTT 720
 Qy 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
 Db 721 ATGGGGATGGCGGTTTATGCGCATCTGGTGTACCTGTACCGACAAACCATGTCGGCAAC 780
 Qy 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
 Db 781 CGTCTGTTGGCATGCTTGGCCAGGCGATGGACGCTTAAAGCGCGCGCAGGATAAGATT 840
 Qy 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
 Db 841 GGCAGGCTGTCGAAGGCTATCGCAATACGAAAGAGTTTCGTGAATTTGGGCGCACCGTTT 900
 Qy 301 GlyValGluMetProIleThrGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
 Db 901 GGTGTTGAAATGCGCAATAACCGAGGAAATTTATCAAGTATTTGTTATTCGGAAAAACGCG 960
 Qy 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
 Db 961 CCGGAGCGCAGCATTAACGTTATTAGTTCGCGCGCGCGAAGGAGAGCTGAGTCGCCAC 1017
 RESULT 6
 ACA31966
 ID ACA31966 standard; DNA; 1017 BP.
 XX
 AC ACA31966;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Prokaryotic essential gene #13623.
 XX
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 XX drug design; gene.
 OS Enterobacter cloacae.
 XX
 FN WO20027183-A2.
 XX

PD 03-OCT-2002.
XX PF
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX P-PSDB; ABU28096.
XX WPI; 2003-029926/02.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 19836; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid;
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
XX prokaryotic essential genes. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1017 BP; 207 A; 289 C; 312 G; 209 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.04e-149 Length: 1017
XX Score: 1635.00 Matches: 319
XX Percent Similarity: 97.35% Conservativity: 11
XX Best Local Similarity: 94.10% Mismatches: 9
XX Query Match: 94.95% Indels: 0
XX DB: 8 Gaps: 0
XX
XX US-10-088-079-2 (1-339) x ACA31966 (1-1017)
XX
XX 1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
XX Db 1 ATGAGCACTGTAATGCGCTCAATGACTGTATCGCGCTCATACGGCACCCTCTT 60
XX
XX 21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40

Db GCCATCAGCTGGCAAGAAATGGTCACGAAGTGGTCTCTGGGGCCACGACCCAAACAT 120
Qy 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
Db 121 ATCGCAACGCTGCAACCGACCGTTGTAAACGTGGCGTTTCTTCCGGAGCGTTCCGTTCC 180
Qy 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
Db 181 GACTCCCTGCACCTTGAAGCGACCTTGGACCGCGCTGGCGGCGGCGGCGGCAACATCTG 240
Qy 81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
Db 241 ATTGTGGTTCGAGCCATGATTTGGGACGCTGCTCGTCAGATTAAAGCCGCTGATGCGC 300
Qy 101 ProAspAlaArgLeuValTrpAlaThrIleGlyLeuGluAlaGluThrGlyValArgLeu 120
Db 301 CCGGATCGCGCATGTGTCTGGGCGACAAAGAGACTGGAAGCCGAAACCGGACGCTGTG 360
Qy 121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
Db 361 CAGGACGTTGCCCGGAGCGCTGGTGATCGGATCCCGCTGGCGGTCATCTCCGGCCCG 420
Qy 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
Db 421 ACCTTTGCCAAGAGCTGGCGCTGGCTGCGACGCGCATTTCCGTGGCTCCACCGAT 480
Qy 161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
Db 481 CAGGCCCTTCTCCGACGATCTTCAACAGCTGCTGCAGCTGGCGCAAGAGCTTCCGGCTTAC 540
Qy 181 SerAsnProAspPheIleGlyValGlnLeuGlyAlaValLysAsnValIleAlaIle 200
Db 541 AGCAACCCCGATTTATTCGGCGTCAACTGGCGCGTGGGTGAGNAGCTGATTCGGATT 600
Qy 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
Db 601 GGCGCCGGGATGTCAAGCGCATTTGGTTGGTGCCAATGCGCTAGCGCTGATCACC 660
Qy 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
Db 661 CGAGGGCTTAACCGAAATGTCCCGCTGGGCGAAGCGCTGGGTGGCGATCCGGCCACCTTT 720
Qy 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
Db 721 ATGGGAATGGCTGGCTGGCGACCTGGTGTGACCTGTACCGATACCCAGTCTCGTAAC 780
Qy 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGlyLysIle 280
Db 781 CGCCGTTTGGCATGTGCTCGACAGCGCAGCGATGTTAAAGGCGGCGGCGGAGAGATT 840
Qy 281 GlyGlnValValGluGlyTyrArgAsnThrIleGluValValArgGluLeuAlaHisArgPhe 300
Db 841 GGTGAGTGGTGTGAAGGCTACCGCAATACCAAGAGTCCGCGAGTTGGCGGACCGCTTTC 900
Qy 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
Db 901 GGTGTCCGAATGCCAATAACCGAGGAATTTATCAGGTATTGTATTGGGAAAAAATCGG 960
Qy 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
Db 961 CGCGAGGCGAGCATTTGACCTATTATTAGTTCGTGGCGGCAAGGAGCGGCGGAGCGTAAC 1017
XX
XX RESULT 7
XX ACA35838
XX ID ACA35838 standard; DNA; 1017 BP.
XX AC
XX AC35838;
XX AC
XX 19-JUN-2003 (first entry)
XX DT
XX Prokaryotic essential gene #17495.
XX DE
XX

Antisense; ds; prokaryotic essential gene; cell proliferation;
drug design; gene.

KW Klebsiella pneumoniae.
KW WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX P-PSDB; ABU31968.
XX WPI; 2003-029926/02.
XX DR P-PSDB; ABU31968.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 14; SEQ ID NO 23708; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pat_sequences
SQ Sequence 1017 BP; 194 A; 306 C; 319 G; 198 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4, 98e-145 Length: 1017
Score: 1587.00 Matches: 313
Percent Similarity: 95.58% Conservative: 11
Best Local Similarity: 92.33% Mismatches: 15
Query Match: 92.16% Indels: 0
DB: 8 Gaps: 0

US-10-088-079-2 (1-339) x ACA35838 (1-1017)
Qy 1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
Db 1 ATGAACGCACCTTAATGCTGCAATGATGCTGATCGTGGCGCTCTTACCGGCACCGCTCTT 60
Qy 21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
Db 61 GCCATCACCTGGCAAGAAATGCCACACGCTTGTGTGGGGCCATGACCCGAAACAT 120
Qy 41 IleAlaThrLeuGluArgAspArgCysAsnAlaPheLeuProAspValProPhePro 60
Db 121 ATCGGACGCTGCAACACGATCGCTGCAACCGCGCTTCTTCCGATGTGCTTCCCG 180
Qy 61 AspThrIleuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
Db 181 GATACGCTGCATCTTGAGAGCGACCTGGCCACCGCTGGCGCGCGACGACATCCTT 240
Qy 81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
Db 241 GTCTGTGTCGCGAGCCATGTAATTCGGTCAAGTGTACGCCAGATTAACCGCTGATCGT 300
Qy 101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
Db 301 TCCGACGCGCGGTGTGTGGGCCACCAAGAGGCTTGAGGCCGNAACCGCGCTCTGTG 360
Qy 121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
Db 361 CAGCAGCTGGCGGTGAAGCGCTGGCGCATATTCGCTGGCGGTGATCTCGGGGCCA 420
Qy 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
Db 421 ACCTTCCCAAGAGCTGGCGCGCTGCCGCGGATTCGCTGGCGGCCACCGAT 480
Qy 161 GlnThrPheAlaAspLeuGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
Db 481 CCGCAGTTTCCGGAGGACCTTCAGCGCTACTGCATCGCGCAAAAGCTTCGCGTCTAC 540
Qy 181 SerAspProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
Db 541 ATCAACCGGACCTTATTCGCGGTGACGTCGCGCGCGCGTGAAGAAACGTCATTGCCATC 600
Qy 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
Db 601 GGGCAGGTATGTGCGACGCACTCGGCTTCGCGGCCAATGCGGTACGCGCTGATTACC 660
Qy 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
Db 661 CGTGGGCTGTGGAAATGTCCCGCTCGCGCGCGCTGGCGCGCGATCCGGAACCTTT 720
Qy 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
Db 721 ATGGGATGGCGCGCTCGGTGACCTCGTGTCTCACCTGCACCGACACACGTCGCGTAAC 780
Qy 261 ArgArgPheGlyMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
Db 781 CGTGGCTTCGGCATGATGCTCGCGCGAGGTATGACGTGCGAGCGCGCCAGGACAGATT 840
Qy 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
Db 841 GGCAGGTGTGTAAGGCTACCGCAATACCAAGGAAGTTCGCGTTCGCGCACACGCTTTA 900
Qy 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
Db 901 GGTGTCGAAATGCGCAATAACCGAGGAATTTATCAGGTATTGATTTCGCGAAAAATTCG 960
Qy 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
Db 961 CGCGAGGACGATTCACCTTATTGGGTGCGCGCGCGCGCGAGGACGCGCGAGCAAT 1017
RESULT 8
ACH97774
ID ACH97774 standard; DNA; 1038 BP.

XX ACH97774;
 AC XX
 DT 29-JUL-2004 (first entry)
 XX Klebsiella pneumoniae polynucleotide seqid 3569.
 DE XX
 KW Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
 XX XX
 OS Klebsiella pneumoniae.
 XX XX
 PN US6610836-B1.
 XX XX
 PD 26-AUG-2003.
 XX XX
 PF 27-JAN-2000; 2000US-00489039.
 XX XX
 PR 29-JAN-1999; 99US-0117747P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX PA
 XX Breton GL, Osborne M;
 XX WPI; 2003-895346/82.
 DR P-PSDB; ABO64223.
 XX XX
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX XX
 PS Disclosure; SEQ ID NO 3569; 932pp; English.
 XX XX
 CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This sequence encodes a Klebsiella
 CC pneumoniae polypeptide of the invention
 XX XX
 SQ Sequence 1038 BP; 201 A; 310 C; 324 G; 203 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,12e-145 Length: 1038
 Score: 1587.00 Matches: 313
 Percent Similarity: 95.58% Conservative: 11
 Best Local Similarity: 92.33% Mismatches: 15
 Query Match: 92.16% Indels: 0
 DB: 11 Gaps: 0
 US-10-088-079-2 (1-339) x ACH97774 (1-1038)
 QY 1 MetAanGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
 DB 19 ATGAACGCACCTTAATGCTGCAATGATGCTGATCGGTGCGGCTCTTACGGCACCGCTCTT 78
 QY 21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTyrGlyHisAspProGluHis 40
 DB 79 GCCATCCCTGGCAAGAAATGCCACACCATGTTGCTGTGGGGCCATGACCCGAAACAT 138
 QY 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
 DB 139 ATCGCGACGCTGCAACACGATCGCTGCAACGCGGTTCTTCCGATGTGCTTTCCTCCG 198
 QY 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
 DB 199 GATACGCTGCATCTTGAGAGCGACCTGGCCACCGCGCTGGCGCGCAGCGGACATCCTT 258
 QY 81 ValValValProSerHisValPheGlyGluValValLeuArgGlnIleLeuProLeuMetArg 100
 DB 259 GTCGGTGGTGGCCAGCCATGATTCGTGAGGTGTTACCGCAGATTAACCCGCTGATGCGT 318
 QY 101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120

Db 319 TCCGACGCGCGCTGGTGTGGCCACCAAGGCTTGGGCGAAACCGCGCTGTGCTG 378
 QY 121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
 Db 379 CAGGACGTGGCGCGCTGAAGCGCTGGCGGATGATATTCGCTGGCGGTGATCTCGGGGCA 438
 QY 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
 Db 439 ACCTTCGCCAAGAGCTGGCGCGCTGGCGGCGGATTCGCTGGCGGCGCACGGAT 498
 QY 161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
 Db 499 CCGCAGTTTGGGAGGACCTTCAGCGCTCTGTCACCTGGCGCAAGCTTCGCGCTCTAC 558
 QY 181 SerAsnProAspPheIleGlyValGlnLeuGlyAlaValLysAsnValIleAlaIle 200
 Db 559 ATCAACCCGGACTTTATCGCGCTGCAGCTCGCGCGCGCGTGAATAAACGTCATTCCCATC 618
 QY 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
 Db 619 GGGGCGATGATGTGGATGGCATCGCTTCGGCGCAATGCGCGTACGCGCTGATTACC 678
 QY 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
 Db 679 CGTGGCTGTGTGAATGTCTCCGCTCGCGCGCGCTGGCGCGCATCCGAAACCTTT 738
 QY 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
 Db 739 ATGGGCATGGCGCGCTCGGTGACCTGCTGCTACCTGCACCGCAACACGATCCCGTAAC 798
 QY 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
 Db 799 CGTGGCTTCGCATGATGCTCGCGCAGGCTATGACGCTGACAGCGCCACGACCAAGATT 858
 QY 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
 Db 859 GGCCAGGTGTGTGAAGGCTACCGCAATACCAAGGAAGTTCCGCTTCTGGCACAGCGTTTA 918
 QY 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
 Db 919 GGTGTCAAAATGCCAATAACCGAGAAATTTTTCAGGTATTGTATTGCGGAAATTCGC 978
 QY 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaAlaArgLysAspGluArgSerSerHis 339
 Db 979 CGCGAGGCGCATTTGACCTTATTGGTTCGCGCGCGCGCGCAGGACGAGCGGCGACGCAAT 1035
 RESULT 9
 ACA49224
 ID ACA49224 standard; DNA; 1023 BP.
 XX ACA49224;
 AC ACA49224;
 XX 19-JUN-2003 (first entry)
 DT XX
 DE Prokaryotic essential gene #30881.
 XX XX
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX XX
 OS Salmonella paratyphi.
 XX XX
 PN W0200277183-A2.
 XX XX
 PD 03-OCT-2002.
 XX XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX FA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-PSDB; ABU45354.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX PT isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 37094; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

XX the 6213 antisense sequences given in the specification where expression

XX of the nucleic acid inhibits proliferation of a cell. Also included are:

XX (1) a vector comprising a promoter operably linked to the nucleic acid

XX encoding a polypeptide whose expression is inhibited by the antisense

XX nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX polypeptide or its fragment whose expression is inhibited by the

XX antisense nucleic acid; (4) an antibody capable of specifically binding

XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX proliferation or the activity of a gene in an operon required for

XX proliferation; (7) identifying a compound that influences the activity of

XX the gene product or that has an activity against a biological pathway

XX required for proliferation, or that inhibits cellular proliferation; (8)

XX identifying a gene required for cellular proliferation or the biological

XX pathway in which a proliferation-required gene or its gene product lies

XX or a gene on which the test compound that inhibits proliferation of an

XX organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX compound's activity; (11) a culture comprising strains in which the gene

XX product is overexpressed or underexpressed; (12) determining the extent

XX to which each of the strains is present in a culture or collection of

XX strains; or (13) identifying the target of a compound that inhibits the

XX proliferation of an organism. The antisense nucleic acids are useful for

XX identifying proteins or screening for homologous nucleic acids required

XX for cellular proliferation to isolate candidate molecules for rational

XX drug discovery programs, or for screening homologous nucleic acids

XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target

XX prokaryotic essential genes. Note: The sequence data for this patent did

XX not form part of the printed specification, but was obtained in

XX electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1023 BP; 219 A; 272 C; 313 G; 219 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.28e-142	Length:	1023
Score:	1556.00	Matches:	318
Percent Similarity:	96.17%	Conservative:	8
Best Local Similarity:	93.81%	Mismatches:	13
Query Match:	90.36%	Indels:	3
DB:	8	Gaps:	0

US-10-088-079-2 (1-339) x ACA49224 (1-1023)

QY 1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20

DB 1 ATGAACCAAGTAAATGCTCAATGACAGTATCGGTGCCGCTGTACGGACCCCT-CTC 59

QY 21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40

DB 60 GCCATCACTCTGGCGAGAACGGCCACAGGTGTCTGTGGGGCCACGACCCCAAAACAT 119

QY 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60

DB 120 ATCGCGACCCCTGGAGCAGATCGGTGCAACGTCTCCGATGTGCTTTCC 179

QY 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80

DB 180 GATACGTTACACCTGGAAAGCGACTTAGCAACCGCGCTGGCGCCAGTCGTAAACATTCGTG 239

QY 81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100

DB 240 GTGGTGGTGCACAGCCATGTTTTCAGCGACGTGTCGGCGAGATTAAACCCGTCATGCGT 299

QY 101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120

DB 300 CCGGATCGCGCTCTGGTATCGGGGACCAAAAGGCTTGAAGCGGAAACGGGGCGCTGTG 359

QY 121 GluAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140

DB 360 CAGGATGTCCTCGCGAAGCGTTAGCGCATCAATCCCGTGGGGGTGATTCTTGGGCCG 419

QY 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160

DB 420 ACGTTCGCTAAAGAAATTTGGCGCGGGTTTTCG-ACGGCAATCTCTCTGGGCTCAACCGAT 478

QY 161 GluThrPheAlaAspLeuGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180

DB 479 GAGACCTTTTCCGACGATCTCCAGCAACTGTTCACCTGCGGAAAGATTTTTCGGGCTAT 538

QY 181 SerAsnProAspPheIleGlyValGlnLeuGlyAlaValLysAsnValIleAlaIle 200

DB 539 ATCAATCGCGATTTTATCGCGCTGCAGCTTGGCGCGCGTGAAGAAAGTATTGCGATT 598

QY 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220

DB 599 GCGCGGGGATGTCTGACGCGATCGGCTTCGGCGCAACGCGCGACGGCTTAATCAGC 658

QY 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240

DB 659 CGTGGAGTACCCAAATGTTCGCGCTTGGCGCAGC-CTTGGCGCGATCCCGCCACCTTT 717

QY 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260

DB 718 ATGGGATGCGGGTTTAGCGGATCTGTGCTGACCTGTACCGACCAACAGTCGCGCAAC 777

QY 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280

DB 778 CGTCGTTTGGCATGATGCTTGGCCAGGCGATGACGTTAAAGGCGCGCAGGATAAGATT 837

QY 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300

DB 838 GCGCAGGTGTGGAAGGCTATCGCAATACCAAGAAAGTTCGTAATTGGCGCACCGTTT 897

QY 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320

DB 898 GGTGTTGAATGCCAATAACCGAGGAATTTATCAAGTTTGTATTCCGGAACAAACGCG 957

QY 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339

DB 958 CGCGAGGCGACATTAAACGTTATTAGTTCGCGCGCGCAAGGAAGAGCTGAGTCGCGCAC 1014

RESULT 10

ACA54019

ID ACA54019 standard; DNA; 1020 BP.

XX AC ACA54019;

XX AC ACA54019;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #35676.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX Yersinia pestis.

XX WO200277183-A2.

XX 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX P-PSDB; ABU50149.
 DR WPI; 2003-029926/02.
 DR P-PSDB; ABU50149.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 41889; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1020 BP; 238 A; 238 C; 288 G; 256 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,69e-132 Length: 1020
 Score: 1455.00 Matches: 283
 Percent Similarity: 91.37% Conservative: 24
 Best Local Similarity: 84.23% Mismatches: 29
 Query Match: 84.45% Indels: 0
 DB: 8 Gaps: 0

US-10-088-079-2 (1-339) x ACM54019 (1-1020)

OY 1 MetAanGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
 DB 1 ATGACACCAACCCCTGCTTCAATGCTGTATCGGTGCGGATCTTACGGCACCGCATTA 60
 OY 21 AlalleThrLeuAlaArgAsnGlyHisGluValValLeuThrGlyHisAspProGluHis 40
 DB 61 GCTATCACACTGGCGCGTAATGGCCATCAAGTCGTGTGTATGGGGCCATGACCTAAACAT 120

OY 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
 DB 121 ATTCACAGCTGCAACAGACCGCTGTAAACCGCGCTTCTACCTGATGCTGCTTTCGCC 180
 OY 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
 DB 181 GATACGTTGCGATTGGAAACCGACTTAGCATGTGCTTGGCTGGCAGCGCGATGTGTG 240
 OY 81 ValValValProSerHisValPheGlyGluValValLeuArgGlnIleLysProLeuMetArg 100
 DB 241 GTCGTGTCGCCACGCCATGCTTTGGTGCTCTTTTACATCAGTTGAACGCCCTCATCTACGT 300
 OY 101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
 DB 301 AAAGATGCAGTATCGCTGCGCAACCAAGGGCTAGAGCTGAAACCGCGCTGTGCTA 360
 OY 121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
 DB 361 CAGGATGTGGCCCGCAAGTCTTGGCGAGGCTATCCGCTTGGCGTGTATTTCTGGTCCA 420
 OY 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
 DB 421 ACGTTCGCCAAAGAAATTTGGCCGCGGTTTGCCTACGGCATTTGGCTTGGCATGCCCAT 480
 OY 161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
 DB 481 GTGCAATTTAGCAAGATCTGCACAGTATTGTCACCTGTGGAAAAGCTTTCGAGTTTAC 540
 OY 181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
 DB 541 AGTAATCTGATTTATCGGGGTACAGCTTGGTGGCGAGTGAAGAAACGTTGATTCGCATC 600
 OY 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
 DB 601 GGTACAGGTATGTCGATGGCATCGGTTTGGTGGCAATGCCCGTACCGCTCTTAATAACC 660
 OY 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
 DB 661 CGCGGGTTAGCGAGATGACCGGCTTAGGGACGCGATTAGTGGCGATCCTTCCACCTTT 720
 OY 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
 DB 721 ATGGGCATGGCAGGGTTAGCGATTTGGTGTAACTGACACAGATAACCAATCCGTAAC 780
 OY 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
 DB 781 CGCCGATTTGGCATTTATGCTGGGTGCGGGTTGGGGGTGAAGGAGCGCGACCAACATT 840
 OY 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
 DB 841 GGTCAAGTGTAGAGGTATACCGTAATACCAAGGAGTTCTGGCATTAGCACACGGTCAT 900
 OY 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
 DB 901 GCGCTCGAAATGCCAATACTGAACAAATTTATCAAGTGTGTATTTGTCATAAGAATGCT 960
 OY 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArg 336
 DB 961 CGTGAGCGGCTGTGACGTGTTTGGGGCGGACCAAAAAAAGATGAAAAA 1008
 RESULT 11
 ADF03046
 ID ADF03046 standard; DNA; 1023 BP.
 XX
 AC ADF03046;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Bacterial polynucleotide #3331.
 XX
 KW Proteus mirabilis infection; bacterial infection; antibacterial;
 KW immunostimulant; gene; ds.

XX OS Proteus mirabilis.
 XX FN US6605709-B1.
 XX PD 12-AUG-2003.
 XX PF 05-APR-2000; 2000US-00543681.
 XX PR 09-APR-1999; 99US-0128706P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Breton GL;
 XX DR WPI; 2003-895291/82.
 XX DR P-PSDB; ADF07218.
 XX PT New Proteus mirabilis polypeptides and polynucleotides, useful as
 PT reagents for diagnosis of bacterial disease, as components of
 PT antibacterial vaccines, as targets for antibacterial drugs, or as
 PT biocontrol agents for plants.
 XX PS Disclosure; SEQ ID NO 3331; 870pp; English.
 CC The invention relates to new Proteus mirabilis polypeptides and
 CC polynucleotides. The invention also relates to antibodies against the
 CC polypeptides, methods for producing the polypeptides, a method of
 CC generating vaccines for immunising an individual against P. mirabilis, a
 CC method for evaluating a compound for the ability to bind a P. mirabilis,
 CC polypeptide and a method for screening test compounds for anti-bacterial
 CC activity. The polypeptides and polynucleotides are useful as molecular
 CC targets for diagnosing, preventing and treating pathological conditions
 CC resulting from bacterial infection, as reagents for diagnosis of
 CC bacterial diseases, as components of antibacterial vaccines, as targets
 CC for antibacterial drugs or as bio-control agents for plants. This
 CC sequence represents a Proteus mirabilis polynucleotide of the invention.
 XX SQ Sequence 1023 BP; 266 A; 206 C; 264 G; 287 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9.56e-129 Length: 1023
 Score: 1420.00 Matches: 275
 Percent Similarity: 90.72% Conservative: 28
 Best Local Similarity: 82.34% Mismatches: 31
 Query Match: 82.46% Indels: 0
 DB: 10 Gaps: 0
 US-10-088-079-2 (1-339) x ADF03046 (1-1023)
 QY 5 AsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeuAlaIleThrLeu 24
 DB 13 AACGCTTCTATGACAGTATTCGGTCCCGGTTTCATACGCGCACCGCTTTAGCGATTACCTTA 72
 QY 25 AlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHisIleAlaThrLeu 44
 DB 73 CGCGTATATGGCAGAGTGTGTCTGTGGGGGATGATCCCAAGCAGCTTCCGCGCATTA 132
 QY 45 GluArgAspArgCysAsnAlaAlaPheLeuProAspValProPheProAspThrLeuHis 64
 DB 133 GAACAAGCGCGCTGTATCAAGCCTTCTCTGCTGATGTTCTCTTCCTGATAGTTATAT 192
 QY 65 LeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeuValValPro 84
 DB 193 ATGGAAGCTTCTTTCGCAAAAAGCATTGAACGCGAGCGGTATATTCCTGTGTGATCCCA 252
 QY 85 SerHisValPheGlyGluValLeuArgGlnIleLeuValMetArgProAspAlaArg 104
 DB 253 AGCCATGTGTGTGTAAGTACTGCAACAATCAACCCCTTTTACGTACGATCGCGGT 312
 QY 105 LeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeuGlnAspValAla 124
 DB 313 GTTGTGTGGCGCAAAAAGGCTTCTGAAGCAGCATACTGTGTCGCTTATTACAAGATGTTGCC 372

QY 125 ArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyProThrPheAlaLys 144
 DB 373 CGTGAAGTATTAGTAAATCCCGCTCGAGTATTCTGGCCCTACTTTTGGCTAAA 432
 QY 145 GluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAspGlnThrPheAla 164
 DB 433 GAGCTTGGCGGGTGTGGCCACCGGATTCGAGTGGCTCGACGGATATCTCTTTTA 492
 QY 165 AspAspLeuGlnLeuLeuHisCysGlyLysSerPheArgValTyrSerAsnProAsp 184
 DB 493 GAGCAGTTACACAGCTATTCTTATTTGGTAAAGTTTCGAGTCTATAAAAACCCCTGAT 552
 QY 185 PheIleGlyValGlnLeuGlyAlaValIleAsnValIleAlaIleGlyAlaGlyMet 204
 DB 553 TTTATCGGTGTCAACTGGGTGGCTGTGTTAAACGCTGATTGCTATTGGTGGGGTATG 612
 QY 205 SerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThrArgGlyLeuAla 224
 DB 613 TCTGATGTTGGATTTGGCGCTAATGCGGTACCGCACTGATTACCGAGGTCTAGCC 672
 QY 225 GluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPheMetGlyMetAla 244
 DB 673 GAAATGAGCGCTTTAGGTAAAGCCTTAGGTGAGTCCAGTCCGCAACTTTTATGGGCATGCT 732
 QY 245 GlyIleGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsnArgArgPheGly 264
 DB 733 GGTTTGGGTGATTTAGTATTTAACTGTACTGACCAACCAATCAGCTAATCGTCGCTCGGT 792
 QY 265 MetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGlnLysIleGlyGlnValVal 284
 DB 793 ATGATGCTAGGTCAAGGTTTAGATGTTGATACGCGCAAGAGAAATTCGCCAGTAGTC 852
 QY 285 GluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPheGlyValGluMet 304
 DB 853 GAAAGTTTATCGTAAACCAAGAAAGTTTCGCGCATTTAGCCGCAACAGGTGGGTGTAGAAATG 912
 QY 305 ProIleThrGluIleThrGlnValLeuValLeuTyrCysGlyLysAsnAlaArgGluAlaAla 324
 DB 913 CCAATCACCAGACAGATCTACCAAAATTTTATATCAATAAAGATGTAAAGAGCGGTGCA 972
 QY 325 LeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSer 338
 DB 973 TTGGCTTTATTAGGCGGAGCAACCAAGATGAGATAGACAGC 1014
 RESULT 12
 ACA44463
 ID ACA44463 standard; DNA; 1011 BP.
 XX AC ACA44463;
 XX DT 19-JUN-2003 (first entry)
 XX DE Prokaryotic essential gene #26120.
 XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 XX KM drug design; gene.
 XX OS Proteus sp.
 XX FN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US0009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PR 06-SEP-2001; 2001US-00948993.
 XX PR 25-OCT-2001; 2001US-0342923P.
 XX PR 08-FEB-2002; 2002US-00072851.
 XX PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX P-PSDB; ABU40593.
 DR WPI: 2003-029926/02.
 DR P-PSDB; ABU40593.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PT Claim 14; SEQ ID NO 32333; 1766pp; English.
 PS
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1011 BP; 260 A; 206 C; 261 G; 284 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7.1e-128 Length: 1011
 Score: 1411.00 Matches: 274
 Percent Similarity: 90.12% Conservative: 27
 Best Local Similarity: 82.04% Mismatches: 33
 Query Match: 81.94% Indels: 0
 DB: 8 Gaps: 0

US-10-088-079-2 (1-339) x ACA44463 (1-1011)

QY 5 AsnAlaSerMetThrValIleGlyValGlySerTyGlyThrAlaLeuAlaIleThrLeu 24
 DB 4 AACGGCTTCTATGACAGTATTCGGTCCGGTTCATACGGCAGCGCTTTAGCGAATACCTTA 63
 QY 25 AlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHisIleAlaThrLeu 44
 DB 64 GCGCGTAATGGGCACGATGTTGTGTGGGGGCATGATCCCAAGCAGCTTGGCGCATTA 123
 QY 45 GluArgAspArgCysAsnAlaAlaPheLeuProAspValProPheProAspThrLeuHis 64
 DB 124 GAACAAGCGCGCTGTAATCAAGCCCTTCTGCCCGATGTTTCCTTCCTGATGTTATAT 183
 QY 65 LeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeuValValPro 84
 DB 184 ATGGAAGCTCTTTTGCAAAAGCGATGTAAGCGCGGTAATATTCTTGTGTGATGCCA 243

QY 85 SerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArgProAspAlaArg 104
 DB 244 AGCCATGTGTTGGTGAAGTACTGCAACAATCAACCCCTTTTACGTCAGGATCGCGT 303
 QY 105 LeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeuGlnAspValAla 124
 DB 304 GTTGTGTTGGGCGCACAAGAGTCTTGAAGCACAATCTGGTTCGCTTATTATCAAGATGTTGCC 363
 QY 125 ArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyProThrPheAlaLys 144
 DB 364 CGTGAAGTATTAGTAATGAATCCGCTCGCAGTATTATCTGGCCCTACTTTTGTCTAAA 423
 QY 145 GluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAspGlnThrPheAla 164
 DB 424 GAGCTTGAGCGGGTATTACCCACCGGATTCAGTGGGCTCGACGGAATACTCTCTTTTA 483
 QY 165 AspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTySerAsnProAsp 184
 DB 484 GAACAGTTTACACAGCTATTCTTNTTGTGTAAAAGCTTCCGAGTCTATATAAACCCTGAT 543
 QY 185 PheIleGlyValGlnLeuGlyGlyValaValLysAsnValIleAlaIleGlyValaGlyMet 204
 DB 544 TTTATCGGTGCAACTGGGGGGGCGCTGTTAAAACGATGCTATTATTTGGTGGCGGTATG 603
 QY 205 SerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThrArgGlyLeuAla 224
 DB 604 TCTGATGTTATGGGATTTGGCGCTAAATGCGCGTACTGTCACCTATTATACCGTGTCTGCC 663
 QY 225 GluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPheMetGlyMetAla 244
 DB 664 GAATATGAGCCGCTTAGGTAAAAGCTTAGGTGCAGATGCGGCACTTTTATGGGCATGGCT 723
 QY 245 GlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsnArgPheGly 264
 DB 724 GGTGTTGGTGTATTAGTTTAACTGTACTGACCAACCAATCAGCTAATCGTCGTTCCGT 783
 QY 265 MetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIleGlyGlnValVal 284
 DB 784 ATGATGCTAGTCAAGGTTTGGTGTGATACAGCCCAAGAGAAAATTTGGCCAGGTAGTC 843
 QY 285 GluGlyTyArgAsnThrLysGluValArgGluLeuAlaHisArgPheGlyValGluMet 304
 DB 844 GAAGGTATATCGTAACCAAGAGTTCGCGCATTTAGCCCAACAGAGTGGTGTAGAAATG 903
 QY 305 ProIleThrGluGluIleTyGlnValLeuTyGlyLysAsnAlaArgGluAlaAla 324
 DB 904 CCAATCACCGAACAGATCTACCAATTTTATATCAACATAAAGATGTTAAAAGAGGCTGCA 963
 QY 325 LeuThrLeuLeuGlyArgAlaAlaArgLysAspGluArgSerSer 338
 DB 964 TTGGCTTTTATAGGCGGAGCAACCAAGATGAGATAGACAGC 1005
 RESULT 13
 ACF70491
 ID ACF70491 standard; DNA; 1023 BP.
 XX
 XX ACF70491;
 AC
 AC ACF70491;
 DT 20-NOV-2003 (first entry)
 XX
 DE Photorhabdus luminescens nucleotide sequence #8958.
 XX
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
 KW detection; food; gene expression; plant; animal; microorganism; toxin;
 KW antibiotic; biopesticide; virulence factor; disease model; plague;
 XX whooping cough; gene; ds.
 OS
 XX Photorhabdus luminescens.
 PN
 XX WO200294867-A2.
 XX
 XX 28-NOV-2002.
 PD

PF 07-FEB-2002; 2002WO-IB003040.
 XX
 PR 07-FEB-2001; 2001FR-00001659.
 XX
 XX (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
 PI Buchrieser C;
 XX
 XX WPI; 2003-148459/14.
 XX
 XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 XX
 XX Claim 2; SEQ ID NO 8958; 1205pp; French.
 XX
 XX The invention relates to the isolation of genes and their encoded
 CC proteins from Photorhabdus luminescens. The isolated sequences are
 CC sources of probes and primers for detecting the genome of P. luminescens
 CC and related species; to study polymorphisms; for gene analysis and for
 CC detection/amplification of the genes. Antibodies (Ab) raised against the
 CC polypeptides encoded by the genes are used for detection/identification
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
 CC carry a gene-containing vector are used to select compounds that
 CC modulate, regulate, induce or inhibit expression of the genes in plants,
 CC animals or microorganisms other than P. luminescens and are able to alter
 CC response or sensitivity to toxins and antibiotics produced by P.
 CC luminescens. Cells transformed to express the genes are useful for
 CC recombinant production of the proteins, particularly toxins and
 CC antibacterials useful as insecticides, bactericides and fungicides. The
 CC genes, proteins, vectors containing the genes and Ab are also useful
 CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which P.
 CC luminescens is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated P. luminescens genes
 XX
 SQ Sequence 1023 BP; 260 A; 197 C; 275 G; 291 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,66e-126 Length: 1023
 Score: 1393.50 Matches: 270
 Percent Similarity: 89.55% Conservative: 30
 Best Local Similarity: 80.60% Mismatches: 34
 Query Match: 80.92% Indels: 1
 DB: 10 Gaps: 1

US-10-088-079-2 (1-339) x ACF70491 (1-1023)

Qy 1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
 Db 1 ATGAATAGT---ACTGTTTCTATGACAGTATTGGTGGCGGCTCATACGGCACCTCATTA 57
 Qy 21 AlaIleThrLeuAlaArgAsnGlyHisGluValValleuThrGlyHisAspProGluHis 40
 Db 58 GCCATTACGCTGGCTCGTAATGGTGCATATGTTGCTACTTTGGGGGCATATCCAGAGCAT 117
 Qy 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
 Db 118 GTTGGGGCATTTGCACCGGTGGTGTGTTAATCAAAATTTCTGCCGGATGTTCTTCCTCT 177
 Qy 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
 Db 178 GATAGTTTATTGCTTGAACCGGACCTAATAAAGCACTTAACAGCGAGCGCGGATATTCTT 237
 Qy 81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
 Db 238 GTTGGGTACCTAGCATGTGTTGGTGAAGTGTAAAGCAGATAAAACCACTTTACGG 297
 Qy 101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120

Db 298 CCTGATTCACGTATCGTATCGGCAACTAAAGGCTTGGAAAGCGGATACCGTTCGGTTATTG 357
 Qy 121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
 Db 358 CAGGATGTGGCCCGTGGATATTAGGCAATGAAATACCGCTAGCGGTCTCTCTGGGCCA 417
 Qy 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
 Db 418 ACATTTCCTAAAGAGTTAGCGGCTGGTTCCTACCGCGATTGCTATTTCGGACCGAA 477
 Qy 161 GlnThrPheAlaAspLeuGlnLeuHisCysGlyLysSerPheArgValTyr 180
 Db 478 TCTGCTTTTGGCGATGACATTCACCAATTATTCACCTGTGGCAAAAGTTTCGGGTTAT 537
 Qy 181 SerAsnProAspPheIleGlyValGlnLeuGlyAlaValLysAsnValIleAlaIle 200
 Db 538 AAAAATCCTGATTTTATTGGTTCCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 597
 Qy 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
 Db 598 GGGCGGGGAATATCTGATGCATGGGATTTGGTGTCTAATGCTGTACCGCATTTGATTACT 657
 Qy 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
 Db 658 CTGGATTTGGGGGAAATGAGTGGCTTGGTGGCAGCGCTTGGTGTCTGATCTCTTACTTT 717
 Qy 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
 Db 718 ATGGCATGCGGGGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 777
 Qy 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
 Db 778 CGTGGTTTGGCATGATGCTGGGGCAGGAAATCAGTGTGAAAGAGCGCATATCAGATT 837
 Qy 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
 Db 838 GGGCAGGTGTTGTAAGTTATCGCAATACCAAGAGTACGTGCAATTGGCTAATCGCGCC 897
 Qy 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
 Db 898 AATGTAGAAATGCGGATTGCAAGCAAAATCTACCAATATCTATTGCAATAAAATGTG 957
 Qy 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGlu 335
 Db 958 ATAGAAGCTGCTCAGGCATTATTAGGAAGAGCCAGAAAGATGAG 1002

RESULT 14
 ACF65374
 ID ACF65374 standard; DNA; 69727 BP.
 XX
 AC ACF65374;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Photorhabdus luminescens nucleotide sequence #27.
 XX
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
 KW detection; food; gene expression; plant; animal; microorganism; toxin;
 KW antibiotic; biopesticide; virulence factor; disease model; plague;
 KW whooping cough; gene; ds.
 XX
 OS Photorhabdus luminescens.
 XX
 FN WO200294867-A2.
 XX
 PD 28-NOV-2002.
 XX
 DP 07-FEB-2002; 2002WO-IB003040.
 XX
 PR 07-FEB-2001; 2001FR-00001659.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.

XX
PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX WPI: 2003-148459/14.
XX
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
XX Claim 1: SEQ ID NO 27; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 69727 BP; 20213 A; 13239 C; 14632 G; 21638 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 9,67e-124 Length: 69727
Score: 1393.50 Matches: 270
Percent Similarity: 89.55% Conservative: 30
Best Local Similarity: 80.60% Mismatches: 34
Query Match: 80.92% Indels: 1
DB: 10 Gaps: 1

US-10-088-079-2 (1-339) x ACF65374 (1-69727)

Qy 1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
Db 54175 ATGAATAGT---ACTGTTTCTATGACAGTGAATTGGTCCGGCTCATACGGCACCTCATTA 54231

Qy 21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTyrGlyHisAspProGluHis 40
Db 54232 GCCATTACGTCGGCTCGTAATGGTCAATATGTTGTAATCGGCGCATTAATCCAGAGCAT 54291

Qy 41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
Db 54292 GTTGGGGCATTCGCAACGGGTGGTGTGAATCAAAAATTTCTGCCGATGTTCTTCTTCT 54351

Qy 61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
Db 54352 GATAGTTATTGCTTTGAAACGACCTAATAAAGCACTAACACGCGAGCGCGATATTCTT 54411

Qy 81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
Db 54412 GTTGGTACCTAGGCATGTTTGGTGAAGTGTAAAGCAGATAAACACCATTTACGG 54471

Qy 101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
Db 54472 CCTGATTACGTCATGATGGCACTAAAGGCTTTGGAAGCGGATACCGGTCGGTTATTG 54531

Qy 121 GlnAspValAlaArgCysGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
Db 54532 CAGGATGTGGCCCGTGAGATATTAGCAATACCAATACCGCTAGCGGTCTCTCTGGGCCA 54591

Qy 141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
Db 54592 ACATTTGCTAAAGAGTTAGCGCTGGTTGGCTACCGCGATTGCTATTATTTCCGCGACGAA 54651

Qy 161 GlnThrPheAlaAspAspLeuGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
Db 54652 TCTGCTTTTGGCGATGGACTTCAACAATATTATCCACTGTGGCAAAAGTTTCCGGGTTTAT 54711

Qy 181 SerAsnProAspPheIleGlyValGlnLeuGlyAlaValLysAsnValIleAlaIle 200
Db 54712 AAAAATCTGATTTTATTGGTGTTCACCTCGTGGTCCGTAATAAAGCGTATCGCCATT 54771

Qy 201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
Db 54772 GCGCGGGAATATCTGATGGCATGGATTGGTGTCTAATGCTCGTACCGCATTTGATTACT 54831

Qy 221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
Db 54832 CGTGGATTGGCGGAATGAGTCGCTTGGTGCAGCGCTTGGTGTGATCTTCTACCTTT 54891

Qy 241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
Db 54892 ATGGGCATGGCGGATTTGGCGATTGGTCTTAACTTGTAACCAATACGATCAGTAAC 54951

Qy 261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluIle 280
Db 54952 CGTCGTTTGGCATGCTGCGGCGAGGAATCAGTGTGTAAGAAGCGCAGTATCAGATT 55011

Qy 281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
Db 55012 GGGCAGGTTGTTGAAGGTTATCGCAATACCAAGAAGATGTCGATTTGGCTTAATCGCGCC 55071

Qy 301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
Db 55072 AATGTAGAAATGCCGATTGCGAGAACAAATCTACCAAGATACTCTATTGCAATAAAATGTG 55131

Qy 321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaAlaArgLysAspGlu 335
Db 55132 ATAGAAGCTGCTCAGGCATTATTAGGAAGAGCCAGCAAGGATGAG 55176

RESULT 15
ACF67367_35
Continuation (36 of 57) of ACF67367 from base 3500001 (Photorhabdus luminescens nucleoti
WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367

WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	1000001	1110000
WP	ACF67367_11	1100001	1210000
WP	ACF67367_12	1200001	1310000
WP	ACF67367_13	1300001	1410000
WP	ACF67367_14	1400001	1510000
WP	ACF67367_15	1500001	1610000
WP	ACF67367_16	1600001	1710000
WP	ACF67367_17	1700001	1810000
WP	ACF67367_18	1800001	1910000
WP	ACF67367_19	1900001	2010000
WP	ACF67367_20	2000001	2110000
WP	ACF67367_21	2100001	2210000
WP	ACF67367_22	2200001	2310000
WP	ACF67367_23	2300001	2410000
WP	ACF67367_24	2400001	2510000
WP	ACF67367_25	2500001	2610000
WP	ACF67367_26	2600001	2710000
WP	ACF67367_27	2700001	2810000

WP	ACF67367_28	2800001	2910000
WP	ACF67367_29	2900001	3010000
WP	ACF67367_30	3000001	3110000
WP	ACF67367_31	3100001	3210000
WP	ACF67367_32	3200001	3310000
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WP	ACF67367_42	4200001	4310000
WP	ACF67367_43	4300001	4410000
WP	ACF67367_44	4400001	4510000
WP	ACF67367_45	4500001	4610000
WP	ACF67367_46	4600001	4710000
WP	ACF67367_47	4700001	4810000
WP	ACF67367_48	4800001	4910000
WP	ACF67367_49	4900001	5010000
WP	ACF67367_50	5000001	5110000
WP	ACF67367_51	5100001	5210000
WP	ACF67367_52	5200001	5310000
WP	ACF67367_53	5300001	5410000
WP	ACF67367_54	5400001	5510000
WP	ACF67367_55	5500001	5610000
WP	ACF67367_56	5600001	5648894

Alignment Scores:

Pred. No.:	1.77e-123	Length:	110000
Score:	1393.50	Matches:	270
Percent Similarity:	89.55%	Conservative:	30
Best Local Similarity:	80.60%	Mismatches:	34
Query Match:	80.92%	Indels:	1
DB:	10	Gaps:	1

US-10-088-079-2 (1-339) x ACF67367_35 (1-110000)

Qy	1	MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu	20
Db	79826	ATGAATAGT---ACTGTTTCTATGACAGTATTGGTCCGGCTATACGGCACCTCATTA	79882
Qy	21	AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis	40
Db	79883	GCCATTACGCTGGCTCGTAATGGTTCATAATCTGTACTTTGGGGGCATAATCCAGAGCAT	79942
Qy	41	IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro	60
Db	79943	GTTGGGGCATTGCAACCGGGTGGTGTGTAATCAAAATTTCTGCCGGATGTTTCCTTTCTCT	80002
Qy	61	AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu	80
Db	80003	GATAGTTATTGCTTGAACCGGACTAATAAAGCACTAAGCAGCGCGCGATATCTT	80062
Qy	81	ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg	100
Db	80063	GTTGTGGTACCTAGCCATGTGTTGGTGAAGCTTAAAGCAGATAAAACCACTATTACGG	80122
Qy	101	ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu	120
Db	80123	CCTGATTACCATGATCGTATGGCAACTAAAGCTTGAAGCGGATACCGGTCGGTTATTG	80182
Qy	121	GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro	140
Db	80183	CAGGATGTGGCCCGTGAATATTAGCAATGAATACCGCTAGCGGTGCTCTCTGGGCCA	80242
Qy	141	ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp	160
Db	80243	ACATTTGCTAAAGAGTTAGCGGCTGGTTGGCTACCGCGATTGCTATTATTTCCGCGACGAA	80302
Qy	161	GlnThrPheAlaAspLeuGlnLeuLeuHisCysGlyLysSerPheArgValTyr	180

Search completed: April 27, 2005, 15:42:11
Job time : 772 secs

Db	80303	TCGCTTTTGGCGATGCACATTCAACAATATTTCACATGTGGCAAAAGTTTCCGGGTTAT	80362
Qy	181	SerAsnProAspPheIleGlyValGlnLeuGlyAlaValLysAsnValIleAlaIle	200
Db	80363	AAAAATCCTGATTTTATTGGTTCACACTCGGTGGTCCGCTAAAAAAGTATGCCCAT	80422
Qy	201	GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr	220
Db	80423	GGCGCGGAATATCTGATGCGATGGGATTTGGTCTAATGCTCGTACCGCATTCATTACT	80482
Qy	221	ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe	240
Db	80483	CGTGGATTGGCGGAATGAGTGGCTTTGGTGCAGCGCTTGGTGTGATCTCTTACCTTT	80542
Qy	241	MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn	260
Db	80543	ATGGGCATGGCGGATTTGGCGGATTTGGTCTTAACCTTGATGATAACCAATCAGCTAAC	80602
Qy	261	ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle	280
Db	80603	CGTCGTTTGGCATGATGCTGGGGCAGGAATCAGTCTTGAAAGAAAGCGCAGTATCAGATT	80662
Qy	281	GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe	300
Db	80663	GGGCAGGTTGTTGAAGGTTATCGCAATACCAAGAAAGTACGTGCAATTGGCTTAATCGCGCC	80722
Qy	301	GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla	320
Db	80723	AATGTAGAAATGCCGATTGCGAACAATCTACCAGATCTCTATTGCAATAAAATGTG	80782
Qy	321	ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGlu	335
Db	80783	ATAGAAGCTGCTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAG	80827

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OM protein - protein search, using sw model

Run on: April 27, 2005, 10:44:58 ; Search time 164 Seconds
(without alignments)
799.462 Million cell updates/sec

Title: US-10-088-079-2

Perfect score: 1722

Sequence: 1 MNORNASMTVIGAGSYGTAL.....AREAAITLLGRKRDERSH 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1722	100.0	339	4	AAB62189 E. coli g
2	1719	99.8	339	2	AAW57330 Glycero-
3	1719	99.8	339	2	AAW60258 Klebsiell
4	1719	99.8	339	2	RAY26172 Glycero-
5	1719	99.8	339	4	AAU34796 E. coli c
6	1719	99.8	339	6	ABU28819 Protein e
7	1719	99.8	339	8	ADS45174 Bacterial
8	1640	95.2	339	6	ABU47465 Protein e
9	1635	94.9	339	6	ABU28096 Protein e
10	1621	94.1	339	6	ABU45354 Protein e
11	1587	92.2	339	6	ABU31968 Protein e
12	1587	92.2	345	7	ABO64223 Klebsiell
13	1455	84.5	339	6	ABU50149 Protein e
14	1420	82.5	340	7	ADF07218 Bacterial
15	1411	81.9	337	6	ABU40593 Protein e
16	1393.5	80.9	341	6	ABM68792 Phototrab
17	1373	79.7	330	8	ADN17703 Bacterial
18	1372	79.7	330	8	ADS42893 Bacterial
19	1242	72.1	344	6	ABU49620 Protein e
20	1192	69.2	337	6	ABU39371 Protein e
21	1150	66.8	335	4	AAU35472 Haemophil
22	1150	66.8	335	6	ABU30312 Protein e
23	806	46.8	329	6	ABU33190 Protein e
24	794.5	46.1	334	8	ADS26951 Bacterial
25	794.5	46.1	334	8	ADS27309 Bacterial

26	794.5	46.1	340	8	ADS26576 Bacterial
27	751.5	43.6	346	8	ADS28582 Bacterial
28	738.5	42.9	334	8	ADN26503 Bacterial
29	720.5	41.8	334	8	ADS27486 Bacterial
30	709.5	41.2	340	6	ABU18125 Protein e
31	703	40.8	332	6	ABU23655 Protein e
32	694	40.3	343	6	ABU25613 Protein e
33	692	40.2	355	6	ABU30030 Protein e
34	692	40.2	356	7	ADC94377 E. faeciu
35	681	39.5	353	7	ADC95426 E. faeciu
36	677.5	39.3	339	7	ADB08818 Alloiococ
37	677.5	39.3	342	6	ADB08820 Alloiococ
38	673	39.1	340	4	AAU35259 Enterococ
39	673	39.1	340	6	ABU14598 Protein e
40	672.5	39.1	338	5	ABB49213 Listeria
41	672.5	39.1	338	6	ABU32661 Protein e
42	672.5	39.1	342	4	AAU33428 Enterococ
43	666.5	38.7	327	6	ADB08816 Alloiococ
44	666.5	38.7	345	8	ADS44752 Bacterial
45	666	38.7	335	6	ABU17729 Protein e

ALIGNMENTS

RESULT 1

AAB62189
ID AAB62189 standard; protein; 339 AA.

XX AC AAB62189;

DT 11-JUN-2001 (first entry)

DE E. coli gpsA2FR protein.

XX Glycerol-3-phosphate dehydrogenase; G3PD; feedback inhibition; oil seed;
KW genetic transformation; fatty acid; glycerolipid; osmotic stress; gpsA;
KW gpsA2FR; allele.

OS Escherichia coli.

XX Key Location/Qualifiers

FT Misc-difference 255

FT /label= D255E

FT /note= "wild-type Asp is replaced with Glu"

XX WO200121820-A1.

PD 29-MAR-2001.

XX 21-SEP-2000; 2000WO-CA001096.

PR 22-SEP-1999; 99US-0155133P.

XX (CANADA) NAT RES COUNCIL CANADA.

PI Zou J, Wei Y, Periappuram C, Selvaraj G, Datla R;

XX WPI; 2001-257996/26.

DR N-PSDB; AAF57428.

XX Manipulating glycerol-3-phosphate metabolism of plant for enhancing
PT stress tolerance, altering fatty acid content in glycerolipids, by
PT expressing in plant feedback defective glycerol-3-phosphate dehydrogenase
PT gene.

XX Claim 15; Fig 1; 39pp; English.

XX The invention provides a method for genetically transforming a plant so
CC that it expresses a heterologous glycerol-3-phosphate dehydrogenase
CC (G3PD) that is less sensitive to feedback inhibition than wild-type G3PD.
CC The method involves providing a vector comprising a DNA sequence encoding
CC G3PD that is less sensitive to feedback inhibition than wild-type G3PD

CC and transforming the plant with the vector. The method is useful for
CC expressing a heterologous G3PD less sensitive to feedback inhibition than
CC wild-type G3PD in an oil seed bearing plant, such as Arabidopsis thaliana
CC or Brassica. The vectors are useful for producing a genetically altered
CC plant having altered fatty acid content in its glycerolipids, especially
CC elevated levels of C16 fatty acids and increased osmotic stress tolerance
CC relative to the wild type. The present sequence represents the E. coli
CC gpaA2FR protein. The gene gpaA2FR is an allele of the E. coli gpaA gene,
CC and encodes an altered version of the GPDH protein defective in feedback
CC inhibition. This gpaA2FR gene can be used in the vectors and method of
CC the invention
XX
SQ Sequence 339 AA;

Query Match 100.0%; Score 1722; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-159;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNQRNASMTVIGAGSYGTALAITLARNHGHEVVLWGHDPHEHATLERDRNCNAFLPDVPPF 60
DB 1 MNQRNASMTVIGAGSYGTALAITLARNHGHEVVLWGHDPHEHATLERDRNCNAFLPDVPPF 60
QY 61 DTLHESDLATALAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLAETGRLL 120
DB 61 DTLHESDLATALAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLAETGRLL 120
QY 121 QDVAREALGQIQIPLAVISGPTFAKELAAGLPTAISLASTDQTTFADDLQQLLHCGKSPRVY 180
DB 121 QDVAREALGQIQIPLAVISGPTFAKELAAGLPTAISLASTDQTTFADDLQQLLHCGKSPRVY 180
QY 181 SNPDFIGVQLGGAVKNNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLAALGADPATF 240
DB 181 SNPDFIGVQLGGAVKNNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLAALGADPATF 240
QY 241 MGMAGLDLVLCTENQSRNRFRGMVGQMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
DB 241 MGMAGLDLVLCTENQSRNRFRGMVGQMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
QY 301 GVEMPTIEEYQVLYCGKNAREAAALTLGRARKDERSH 339
DB 301 GVEMPTIEEYQVLYCGKNAREAAALTLGRARKDERSH 339

RESULT 2
AAW57330
ID AAW57330 standard; protein; 339 AA.
AC AAW57330;
XX
XX 14-SEP-1998 (first entry)
XX Glycerol-3-phosphate dehydrogenase gpsA.
XX Glycerol-3-phosphate dehydrogenase; G3PDH; gpaA; yeast.
XX Saccharomyces sp.
XX WO9821340-A1.
XX 22-MAY-1998.
XX 10-NOV-1997; 97WO-US020293.
XX 13-NOV-1996; 96US-0030602P.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX (GEMV) GENENCOR INT INC.
XX Bulthuis BA, Gatenby AA, Haynie SL, Hsu AK, Lareau RD;
XX WPI; 1998-297943/26.
XX Fermentative production of glycerol using recombinant host - containing

PT genes for glycerol-3-phosphate dehydrogenase and/or glycerol-3-
PT phosphate.
XX
XX Claim 9; Page 36-37; 57pp; English.
XX
XX This claimed Saccharomyces polypeptide comprises a glycerol-3-phosphate
CC dehydrogenase (G3PDH) that catalyses the conversion of dihydroxyacetone
CC phosphate to glycerol-3-phosphate. It is encoded by the gpaA gene. The
CC invention provides recombinant organisms that express G3PDH and/or
CC glycerol-3-phosphate (G3P) (see also AAW57324-32) useful for the
CC production of glycerol from a variety of C-sources. A host cell is
CC preferably transformed with a cassette containing either a G3PDH gene
CC and/or a G3P gene and then cultured in the presence of a mono-, oligo-,
CC polysaccharide or LC-substrate. The glycerol obtained is used in
CC cosmetics, liquid soaps, pharmaceuticals, lubricants and antifreezes; its
CC esters are used in the oil and fat industries. The method produces
CC glycerol rapidly and inexpensively without generation of polluting by-
CC products
XX
SQ Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 2; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNQRNASMTVIGAGSYGTALAITLARNHGHEVVLWGHDPHEHATLERDRNCNAFLPDVPPF 60
DB 1 MNQRNASMTVIGAGSYGTALAITLARNHGHEVVLWGHDPHEHATLERDRNCNAFLPDVPPF 60
QY 61 DTLHESDLATALAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLAETGRLL 120
DB 61 DTLHESDLATALAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLAETGRLL 120
QY 121 QDVAREALGQIQIPLAVISGPTFAKELAAGLPTAISLASTDQTTFADDLQQLLHCGKSPRVY 180
DB 121 QDVAREALGQIQIPLAVISGPTFAKELAAGLPTAISLASTDQTTFADDLQQLLHCGKSPRVY 180
QY 181 SNPDFIGVQLGGAVKNNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLAALGADPATF 240
DB 181 SNPDFIGVQLGGAVKNNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLAALGADPATF 240
QY 241 MGMAGLDLVLCTENQSRNRFRGMVGQMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
DB 241 MGMAGLDLVLCTENQSRNRFRGMVGQMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
QY 301 GVEMPTIEEYQVLYCGKNAREAAALTLGRARKDERSH 339
DB 301 GVEMPTIEEYQVLYCGKNAREAAALTLGRARKDERSH 339

RESULT 3
AAW60258
ID AAW60258 standard; protein; 339 AA.
XX
XX AAW60258;
XX
XX 28-SEP-1998 (first entry)
XX Klebsiella pneumoniae glycerol-3-phosphate dehydrogenase.
XX Klebsiella pneumoniae glycerol-3-phosphate dehydrogenase.
XX glycerol-3-phosphate dehydrogenase; production; 1,3-propanediol;
XX recombinant.
XX Klebsiella pneumoniae.
XX WO9821341-A2.
XX 22-MAY-1998.
XX 13-NOV-1997; 97WO-US020873.
XX 13-NOV-1996; 96US-0030601P.
XX

PA (GEMV) GENENCOR INT INC.
 XX Dunn-Coleman NS, Diaz-Torres M, Chase MW, Trimbur D;
 XX WPI; 1998-297944/26.
 DR
 XX New method for increasing production of 1,3-propanediol - comprises
 PT fermentation of inexpensive carbon sources by microorganism expressing
 PT dehydratase, used, e.g. to prolong half-life of enzyme.
 XX
 XX Disclosure; Page 70-71; 133pp; English.
 XX
 CC The sequence is that of glycerol-3-phosphate dehydrogenase. It was used
 CC as part of a method of fermentative production of 1,3-propanediol (1,3-
 CC pd), using an organism comprising at least 1 gene encoding a dehydratase,
 CC is improved by inserting into the host a gene encoding protein X and
 CC culturing the transformant in presence of a carbon source (e.g. mono-,
 CC oligo- or poly-saccharide or 1C substrate) convertible to 1,3-pd. 1,3-pd
 CC is a starting material for polyesters, polyurethanes and cyclic
 CC compounds. 1,3-pd can now be produced by a single recombinant organism
 CC from inexpensive carbon sources such as glucose (rather than costly
 CC glycerol or dihydroxyacetone), rapidly and without causing pollution
 XX
 XX Sequence 339 AA;
 SQ
 Query Match 99.8%; Score 1719; DB 2; Length 339;
 Best Local Similarity 99.7%; Pred. No. 1.4e-158;
 Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNQRNASTVIGAGSYGTALAITLARNHGVVWGHDPHEIATLERDRCNAAFLPDVPPF 60
 DB 1 MNQRNASTVIGAGSYGTALAITLARNHGVVWGHDPHEIATLERDRCNAAFLPDVPPF 60
 QY 61 DTLHESDLATALAASRNILVVPVSHVGEVLRQIKPLMRDPARLVWATKGLEATGRLL 120
 DB 61 DTLHESDLATALAASRNILVVPVSHVGEVLRQIKPLMRDPARLVWATKGLEATGRLL 120
 QY 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVY 180
 DB 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVY 180
 QY 181 SNPDFIGVQLGGAVKNVIAIGAGMSDGI GFGANARTALITRGLAEMSRIGALGADPATF 240
 DB 181 SNPDFIGVQLGGAVKNVIAIGAGMSDGI GFGANARTALITRGLAEMSRIGALGADPATF 240
 QY 241 MGMAGLDLVLTCTENOSRNRFFGMVGGQMDVQSAQEKI GOVVEGYNTKEVRELAHRF 300
 DB 241 MGMAGLDLVLTCTENOSRNRFFGMVGGQMDVQSAQEKI GOVVEGYNTKEVRELAHRF 300
 QY 301 GVEMPTIEEIVQVLYCGKNAREAAALTLGRARKDERSH 339
 DB 301 GVEMPTIEEIVQVLYCGKNAREAAALTLGRARKDERSH 339
 RESULT 4
 AAY26172
 ID AAY26172 standard; protein; 339 AA.
 XX
 AC AAY26172;
 XX
 DT 29-SEP-1999 (first entry)
 XX
 DE Glycerol-3-phosphate dehydrogenase encoded by gpsA gene.
 XX
 KW G3PDH; glycerol-3-phosphate dehydrogenase; NADPH-dependent enzyme;
 KW EC 1.1.1.94; glycerol; recombinant organism; transformation; gpsA gene;
 KW glycerol biosynthetic pathway; expression cassette; 1-3 propanediol;
 KW pharmaceutical compound; antifreeze solution; lubricant; polyurethane;
 KW cyclic compound; fat and oil industry; polyester fiber.
 XX
 OS Saccharomyces sp.
 XX
 PN WO9928480-A1.

XX 10-JUN-1999.
 PD
 XX 02-DEC-1998; 98WO-US025551.
 PF
 XX 02-DEC-1997; 97US-00982783.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (GEMV) GENENCOR INT INC.
 XX
 PI Nair RV, Payne MS, Trimbur DE, Valle F;
 XX
 XX WPI; 1999-385384/32.
 DR
 XX Recombinant organisms containing G3PDH and or G3P phosphatase.
 PT
 XX Claim 12; Page 63-64; 84pp; English.
 PS
 XX The present sequence is a glycerol-3-phosphate dehydrogenase (G3PDH)
 CC enzyme (EC 1.1.1.94) which is NADPH dependent, and catalyses the
 CC conversion of dihydroxyacetone phosphate to glycerol-3-phosphate. This is
 CC encoded by gps A gene. This is used to produce glycerol from a
 CC recombinant organism by transforming a suitable host cell with an
 CC expression cassette comprising either one or both of the genes encoding
 CC G3PDH and G3P, where the host cell has disruptions in either glycerol
 CC kinase or glycerol dehydrogenase endogenous genes to prevent their active
 CC expression. The transformed host cell is cultured with a carbon source
 CC and glycerol is recovered. Compounds derived from the glycerol
 CC biosynthetic pathway like 1,3-propanediol can also be produced. The
 CC method provides a rapid, inexpensive and environment-friendly source of
 CC glycerol. Glycerol is used in cosmetics, food, pharmaceuticals,
 CC lubricants, anti-freeze solutions, fat and oil industry etc. 1,3 -
 CC propanediol is used for the production of polyester fibers and the
 CC manufacture of polyurethanes and cyclic compounds
 XX
 XX Sequence 339 AA;
 SQ
 Query Match 99.8%; Score 1719; DB 2; Length 339;
 Best Local Similarity 99.7%; Pred. No. 1.4e-158;
 Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNQRNASTVIGAGSYGTALAITLARNHGVVWGHDPHEIATLERDRCNAAFLPDVPPF 60
 DB 1 MNQRNASTVIGAGSYGTALAITLARNHGVVWGHDPHEIATLERDRCNAAFLPDVPPF 60
 QY 61 DTLHESDLATALAASRNILVVPVSHVGEVLRQIKPLMRDPARLVWATKGLEATGRLL 120
 DB 61 DTLHESDLATALAASRNILVVPVSHVGEVLRQIKPLMRDPARLVWATKGLEATGRLL 120
 QY 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVY 180
 DB 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVY 180
 QY 181 SNPDFIGVQLGGAVKNVIAIGAGMSDGI GFGANARTALITRGLAEMSRIGALGADPATF 240
 DB 181 SNPDFIGVQLGGAVKNVIAIGAGMSDGI GFGANARTALITRGLAEMSRIGALGADPATF 240
 QY 241 MGMAGLDLVLTCTENOSRNRFFGMVGGQMDVQSAQEKI GOVVEGYNTKEVRELAHRF 300
 DB 241 MGMAGLDLVLTCTENOSRNRFFGMVGGQMDVQSAQEKI GOVVEGYNTKEVRELAHRF 300
 QY 301 GVEMPTIEEIVQVLYCGKNAREAAALTLGRARKDERSH 339
 DB 301 GVEMPTIEEIVQVLYCGKNAREAAALTLGRARKDERSH 339
 RESULT 5
 AAU34796
 ID AAU34796 standard; protein; 339 AA.
 XX
 AC AAU34796;
 XX
 DT 14-FEB-2002 (first entry)

```

XX DE E. coli cellular proliferation protein #377.
XX
XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX KW antibacterial; drug design.
XX
XX OS Escherichia coli.
XX
XX PN WO200170955-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009180.
XX
XX PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
XX PA (ELIT-) ELITRA PHARM INC.
XX
XX PI Haselbeck R, Ohlssen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RI, Xu HH;
XX
XX DR WPI; 2001-611495/70.
XX DR N-PSDB; AAS52655.
XX
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX PS Example 3; SEQ ID NO 10389; 511pp; English.
XX
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the genes,
XX CC their use in the discovery of novel antibiotics, the essential genes
XX CC themselves and the encoded proteins. The prokaryotes used are Escherichia
XX CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX CC useful for the identification of potential new targets for antibiotic
XX CC development. The antisense nucleic acids can also be used to identify
XX CC proteins used in proliferation, to express these proteins, and to obtain
XX CC antibodies capable of binding to the expressed proteins. The proteins can
XX CC be used to screen compounds in rational drug discovery programmes. The
XX CC antisense nucleic acid sequence is also useful to screen for homologous
XX CC nucleic acids which are required for cell proliferation in a wide variety
XX CC of organisms. The present sequence represents an essential prokaryotic
XX CC cellular proliferation protein. Note: The sequence data for this patent
XX CC did not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 4; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNQNASMTVIGAGSYGTALAITLARNHGHEVVLWGHDPDEHATLERDPCNAFLPDVPPF 60
Db 1 MNQNASMTVIGAGSYGTALAITLARNHGHEVVLWGHDPDEHATLERDPCNAFLPDVPPF 60
Qy 61 DTLHLESDATALAASRNILVVVPSHVFEVLROIKPLMRPDARILVWATKGLAEATGRLL 120
Db 61 DTLHLESDATALAASRNILVVVPSHVFEVLROIKPLMRPDARILVWATKGLAEATGRLL 120
Qy 121 QDVAREALGDOIPLAVISGPTFAKELAGLPTAISLASTDTQTFADDLQQLHCGKSRFVY 180
Db 121 QDVAREALGDOIPLAVISGPTFAKELAGLPTAISLASTDTQTFADDLQQLHCGKSRFVY 180
Qy 181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSLGALGADPATF 240

```

181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSLGALGADPATF 240

241 MEMAGLGDVLVTCTTENQSRNRFFGMMLGQGMVQSAQEKIQVVVEGYRNTKEVRELAHRF 300

241 MEMAGLGDVLVTCTDQSRNRFFGMMLGQGMVQSAQEKIQVVVEGYRNTKEVRELAHRF 300

301 GVEMPTIEEIVQVLYCGKNAREAAALTLGLRARKDERSH 339

301 GVEMPTIEEIVQVLYCGKNAREAAALTLGLRARKDERSH 339

RESULT 6

ABU28819

ID ABU28819 standard; protein; 339 AA.

XX AC ABU28819;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #14346.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Escherichia coli.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlssen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA32689.

XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 56743; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX

Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 6; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPHEIATLERDRCNAAFLPDVPPF 60
DB 1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPHEIATLERDRCNAAFLPDVPPF 60
QY 61 DTLHLESDLATATAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
DB 61 DTLHLESDLATATAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
QY 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSPRVY 180
DB 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSPRVY 180
QY 181 SNPDFIGVOLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSLGALGADPATF 240
DB 181 SNPDFIGVOLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSLGALGADPATF 240
QY 241 MGMAGLGDVLVTCTENQSRNRRFCMMLGQGMVQSAQEKIGQVVEGYNTKEVRELAHRF 300
DB 241 MGMAGLGDVLVTCTENQSRNRRFCMMLGQGMVQSAQEKIGQVVEGYNTKEVRELAHRF 300
QY 301 GVEMPTIEEIVQVLYCGKNAREAAITLLGRARKDERSH 339
DB 301 GVEMPTIEEIVQVLYCGKNAREAAITLLGRARKDERSH 339

RESULT 7

ADS45174

ID ADS45174 standard; protein; 339 AA.

AC ADS45174;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #23604.

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX

(CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

DR New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
PT
PT
XX
XX Claim 1; SEQ ID NO 23604; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 8; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPHEIATLERDRCNAAFLPDVPPF 60
DB 1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPHEIATLERDRCNAAFLPDVPPF 60
QY 61 DTLHLESDLATATAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
DB 61 DTLHLESDLATATAASRNILVVPSHVFGVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
QY 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSPRVY 180
DB 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSPRVY 180
QY 181 SNPDFIGVOLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSLGALGADPATF 240
DB 181 SNPDFIGVOLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSLGALGADPATF 240
QY 241 MGMAGLGDVLVTCTENQSRNRRFCMMLGQGMVQSAQEKIGQVVEGYNTKEVRELAHRF 300
DB 241 MGMAGLGDVLVTCTENQSRNRRFCMMLGQGMVQSAQEKIGQVVEGYNTKEVRELAHRF 300
QY 301 GVEMPTIEEIVQVLYCGKNAREAAITLLGRARKDERSH 339
DB 301 GVEMPTIEEIVQVLYCGKNAREAAITLLGRARKDERSH 339

RESULT 8

ABU47465

ID ABU47465 standard; protein; 339 AA.

XX

AC ABU47465;
 XX 19-JUN-2003 (first entry)
 DT Protein encoded by Prokaryotic essential gene #32992.
 XX
 DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 KW Salmomella typhi.
 XX
 OS WO200277183-A2.
 XX
 FN 03-OCT-2002.
 XX
 PD 21-MAR-2002; 2002WO-US009107.
 XX
 PF 21-MAR-2001; 2001US-00815242.
 XX
 PR 06-SEP-2001; 2001US-00948993.
 XX
 PR 25-OCT-2001; 2001US-0342923P.
 XX
 PR 08-FEB-2002; 2002US-00072851.
 XX
 PR 06-MAR-2002; 2002US-00362699P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 XX
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 XX
 DR N-PSDB; ACAS1335.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 FT isolate candidate molecules for rational drug discovery programs.
 XX
 XX Claim 25; SEQ ID NO 75389; 1766pp; English.
 XX
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 339 AA;
 SQ
 Query Match 95.2%; Score 1640; DB 6; Length 339;
 Best Local Similarity 94.7%; Pred. No. 7e-151;
 Matches 321; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNQNASMTVIGAGSYGTALAITLARNHGVVWGHDPKHIAITLERDRCNAAFLPDVPPF 60
 DB 1 MNQNASMTVIGAGSYGTALAITLARNHGVVWGHDPKHIAITLERDRCNAAFLPDVPPF 60
 QY 61 DTLHLSDLATALAASRNILVVVPSHVFGVLRQIKPLMRPDARLVWATKGLAETGRLL 120
 DB 61 DTLHLSDLATALAASRNILVVVPSHVFGVLRQIKPLMRPDARLVWATKGLAETGRLL 120
 QY 121 QDVAREALGQIPLAVISGPTFAKELAAAGLPTAISLASTDQTFADDIQLLHCGKSPRVY 180
 DB 121 QDVAREALGQIPLAVISGPTFAKELAAAGLPTAISLASTDQTFADDIQLLHCGKSPRVY 180
 QY 181 SNPDFTGVQLGGAVKXNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLGAALGADPATF 240
 DB 181 INADFTGVQLGGAVKXNVIAIGAGMSDGI GFANARTALITRGLAEMSRGLGAALGADPATF 240
 QY 241 MGMAGLGLDLVLTCTENQSRNRRFGMLGQGMVQSAQEKIGQVVEGYRNTKEVRELARHF 300
 DB 241 MGMAGLGLDLVLTCTENQSRNRRFGMLGQGMVQSAQEKIGQVVEGYRNTKEVRELARHF 300
 QY 301 GVEMPTTEIYQVLYCGKNAREAAALTLLGRARKDERSH 339
 DB 301 GVEMPTTEIYQVLYCGKNAREAAALTLLGRARKDERSH 339
 RESULT 9
 ABU28096
 ID ABU28096 standard; protein; 339 AA.
 XX
 AC ABU28096;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #13623.
 XX
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Enterobacter cloacae.
 OS
 XX WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 XX 21-MAR-2002; 2002WO-US009107.
 PF
 XX 21-MAR-2001; 2001US-00815242.
 PR
 PR 06-SEP-2001; 2001US-00948993.
 PR
 PR 25-OCT-2001; 2001US-0342923P.
 PR
 PR 08-FEB-2002; 2002US-00072851.
 PR
 PR 06-MAR-2002; 2002US-00362699P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 XX
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 XX
 DR N-PSDB; ACAS1966.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 FT isolate candidate molecules for rational drug discovery programs.
 XX
 XX Claim 25; SEQ ID NO 56020; 1766pp; English.
 XX
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 339 AA;
 SQ
 Query Match 95.2%; Score 1640; DB 6; Length 339;
 Best Local Similarity 94.7%; Pred. No. 7e-151;
 Matches 321; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 181 SNPDFIGVQLGGAVKNNVIAIGAGSDGIGFANARTALITRGLAEMSRGLGALGADPATF 240
 Db 181 INADFIGVQLGGAVKNNVIAIGAGSDGIGFANARTALITRGLAEMSRGLGALGADPATF 240
 QY 241 MGMAGLGDVLVTCTENQSRNRRFCMMLGQGMVDVQSAQEKIGQVVEGYRNTKEVRELAHFR 300
 Db 241 MGMAGLGDVLVTCTENQSRNRRFCMMLGQGMVDVQSAQEKIGQVVEGYRNTKEVRELAHFR 300
 QY 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339
 Db 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339

RESULT 11

ABU31968
 ID ABU31968 standard; protein; 339 AA.

AC ABU31968;

XX 19-JUN-2003 (first entry)

XX Protein encoded by prokaryotic essential gene #17495.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Klebsiella pneumoniae.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA35838.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 59892; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

XX the 6213 antisense sequences given in the specification where expression

XX of the nucleic acid inhibits proliferation of a cell. Also included are:

XX (1) a vector comprising a promoter operably linked to the nucleic acid

XX encoding a polypeptide whose expression is inhibited by the antisense

XX nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX polypeptide or its fragment whose expression is inhibited by the

XX antisense nucleic acid; (4) an antibody capable of specifically binding

XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX proliferation or the activity of a gene in an operon required for

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence is obtained by one of

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 339 AA;

XX Query Match 92.2%; Score 1587; DB 6; Length 339;

XX Best Local Similarity 92.3%; Pred. No. 1e-145;

XX Matches 313; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 MNQNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPKHATLERDRCAAEFLPDVFPF 60

Db 1 MNALNAAMTVIGAGSYGTALAITLARNGHEVVLWGHDPKHATLQHORCAAEFLPDVFPF 60

QY 61 DTLHESDLATALAASRNILVVPVSHVFGVQLRQIKPLMRPDARLVWATKLEAETGRLL 120

Db 61 DTLHESDLATALAASRDILVVPVSHVFGVQLRQIKPLMRSDARLVWATKLEAETGRLL 120

QY 121 QDVAREALGDOIPLAVISGPTFAKELAAGLPTAISLASTDOTFADDIQLLHCGKSPRVY 180

Db 121 QDVAREALGDDIPLAVISGPTFAKELAAGLPTAISLAATDPQAEIDLRLHCGKSPRVY 180

QY 181 SNPDFIGVQLGGAVKNNVIAIGAGSDGIGFANARTALITRGLAEMSRGLGALGADPATF 240

Db 181 INPDFIGVQLGGAVKNNVIAIGAGSDGIGFANARTALITRGLAEMSRGLGALGADPATF 240

QY 241 MGMAGLGDVLVTCTENQSRNRRFCMMLGQGMVDVQSAQEKIGQVVEGYRNTKEVRELAHFR 300

Db 241 MGMAGLGDVLVTCTENQSRNRRFCMMLGQGMVDVQSAQEKIGQVVEGYRNTKEVRELAHFR 300

QY 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339

Db 301 GVEMPTTEIYQVLYCGKNAREAAALTLGRARKDERSH 339

RESULT 12

ABO64223

ID ABO64223 standard; protein; 345 AA.

XX ABO64223;

XX AC ABO64223;

XX 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 10740.

XX Recombinant expression vector; transcription regulatory element;

XX Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX Klebsiella pneumoniae.

XX US6610836-B1.

XX 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

XX 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL, Osborne M;

XX WPI; 2003-895346/82.

XX N-PSDB; ACH97774.

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.

XX
PS Disclosure; SEQ ID NO 10740; 932pp; English.

XX
CC The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention

XX
SQ Sequence 345 AA;

Query Match 92.2%; Score 1587; DB 7; Length 345;
Best Local Similarity 92.3%; Pred. No. 1.1e-145; Mismatches 15; Indels 0; Gaps 0;

Matches 313; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 MNQRNMTVIGAGSYGTALAITLARNHGHEVVLWGHDPKHIAITLDRDRCNAAFLPDVPPP 60

Db 7 MNALNAAMTVIGAGSYGTALAITLARNHGHEVVLWGHDPKHIAITLDRDRCNAAFLPDVPPP 66

QY 61 DTLHLESDLATLAASRNILVVPVSHVFGVLRQIKPLMRPDPARLVWATKGLAEATGRLL 120

Db 67 DTLHLESDLATLAASRDILVVPVSHVFGVLRQIKPLMRSDARLVWATKGLAEATGRLL 126

QY 121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVY 180

Db 127 QDVAREALGDDIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVY 186

QY 181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSRIGALGADPATF 240

Db 187 INPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLVEMSRIGALGADPATF 246

QY 241 MGMAGLDLVLCTCTNQSRNRRFGMMLGQGMVQSAQEKIGQVVGYNTEKRELAHRF 300

Db 247 MGMAGLDLVLCTCTNQSRNRRFGMMLGQGMVQSAQEKIGQVVGYNTEKRELAHRF 306

QY 301 GVEMPTITEIYQVLYCGKNAREAAATLLGRARKDERSH 339

Db 307 GVEMPTITEIYQVLYCGKIAREAAATLLGRARKDERSN 345

RESULT 13

ABUS0149

ID ABUS0149 standard; protein; 339 AA.

XX AC ABUS0149;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #35676.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Yersinia pestis.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX XX 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX DR N-PSDB; ACA54019.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX
PS Claim 25; SEQ ID NO 78073; 1766pp; English.

XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid;
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 339 AA;

Query Match 84.5%; Score 1455; DB 6; Length 339;

Best Local Similarity 84.2%; Pred. No. 7.5e-133;

Matches 283; Conservative 24; Mismatches 29; Indels 0; Gaps 0;

QY 1 MNQRNMTVIGAGSYGTALAITLARNHGHEVVLWGHDPKHIAITLDRDRCNAAFLPDVPPP 60

Db 1 MNTNPASWAVIGAGSYGTALAITLARNHGHEVVLWGHDPKHIAITLDRDRCNAAFLPDVPPP 60

QY 61 DTLHLESDLATLAASRNILVVPVSHVFGVLRQIKPLMRPDPARLVWATKGLAEATGRLL 120

Db 61 DTLHLESDLATLAASRDILVVPVSHVFGVLRQIKPLMRPDPARLVWATKGLAEATGRLL 120

QY 121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVY 180

Db 121 QDVAREALGDAIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVY 180

QY 181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSRIGALGADPATF 240

Db 181 SNPDFIGVQLGGAVKNVIAIGAGSDGIGFGANARTALITRGLAEMSRIGALGADPATF 240

QY 241 MGMAGLDLVLCTCTNQSRNRRFGMMLGQGMVQSAQEKIGQVVGYNTEKRELAHRF 300

Db 241 MGMAGLDLVLCTCTNQSRNRRFGMMLGQGMVQSAQEKIGQVVGYNTEKRELAHRF 300

QY 301 GVEMPTITEIYQVLYCGKNAREAAATLLGRARKD 336

Db 301 GVEMPTITEIYQVLYCHKNAREAAATLLGRARKD 336

RESULT 14
ADF07218
ID ADF07218 standard; protein; 340 AA.
XX
XX ADF07218;
AC ADF07218;
DT 12-FEB-2004 (first entry)
XX
XX Bacterial polypeptide #3331.
DE
XX
XX Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant.
XX
XX Proteus mirabilis.
OS
XX
XX US6605709-B1.
PN
XX
XX 12-AUG-2003.
PD
XX
XX 05-APR-2000; 2000US-00543681.
PF
XX
XX 09-APR-1999; 99US-0128706P.
PR
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
XX Breton GL;
PI
XX
XX WPI; 2003-895291/82.
DR N-PSDB; ADF03046.
XX
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
XX Disclosure; SEQ ID NO 7503; 870pp; English.
PS
XX
XX The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
SQ Sequence 340 AA;
Query Match 82.5%; Score 1420; DB 7; Length 340;
Best Local Similarity 82.3%; Pred. No. 2e-129;
Matches 275; Conservative 28; Mismatches 31; Indels 0; Gaps 0;
QY 5 NASMTVIGAGSYGTALAITLARNQHEVVLWGHDPHEHTATLDRDRCNAAFLPDVPPDTLH 64
DB 5 NASMTVIGAGSYGTALAITLARNQHDVVLWGHDPKHVAALQARCNQAFLDVSPDLSLY 64
QY 65 LESDLATALASRNILVVPVSHVFEVLRQIKPLMRPDLARLVWATKGLEASTGRLLQDVA 124
DB 65 MEASLQKAIEASRNILVVPVSHVFEVLRQIKPLMRPDLARLVWATKGLEASTGRLLQDVA 124
QY 125 REALGDQIPLAVISGPTFAKELAGLPTAISLASTDQTFADDLQQLHCGSRVYSNPD 184
DB 125 REVLGNEIPLAVISGPTFAKELAGLPTAISLASTDQTFADDLQQLHCGSRVYSNPD 184
QY 185 FIGVLGGVKNVIAIGAGSDGIGFGANARTALITRGLAEMSLRGLAALGADPATPFMGMA 244
DB 185 FIGVLGGVKNVIAIGAGSDGIGFGANARTALITRGLAEMSLRGLAALGADPATPFMGMA 244

QY 245 GLGDLVLTCTENQSRNRRFGMLGQGMVDSQAQBKIQGVVEGYNTKEVRELAHRFGVEM 304
DB 245 GLGDLVLTCTDNQSRNRRFGMLGQGLDVTDAQBKIQGVVEGYNTKEVRELAHRFGVEM 304
QY 305 PITTEIYOVLYCKGNAREEALTLGLGRKDERSS 338
DB 305 PITTEIYOVLYCKGNAREEALTLGLGRKDERSS 338
RESULT 15
ABU40593
ID ABU40593 standard; protein; 337 AA.
XX
XX AC ABU40593;
XX
XX 19-JUN-2003 (first entry)
DT
XX
XX Protein encoded by Prokaryotic essential gene #26120.
DE
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW
XX
XX Proteus sp.
OS
XX
XX WO200277183-A2.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 21-MAR-2002; 2002WO-US009107.
PF
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITFA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI: 2003-029926/02.
DR N-PSDB; ACA44463.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 68517; 1766pp; English.
PS
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ

Sequence 337 AA;

Query Match	81.9%	Score 1411;	DB 6;	Length 337;
Best Local Similarity	82.0%	Pred. No. 1.5e-128;		
Matches 274;	Conservative 27;	Mismatches 33;	Indels 0;	Gaps 0;
Qy	5	NASMTVIGAGSYGTALITLARNHGVVLWGHDPKHVLALEQARCNQAFLPDVSPPDLH	64	
Db	2	NASMTVIGAGSYGTALITLARNHGVVLWGHDPKHVLALEQARCNQAFLPDVSPPDLH	61	
Qy	65	LESDLATLAASRNILVVPSPHVFGEVLQIKPLMRPDARLVWATKGLEAETGRLLQDVA	124	
Db	62	MEASLQKAIEASRNILVVPSPHVFGEVLQIKPLMRPDARLVWATKGLEAETGRLLQDVA	121	
Qy	125	REALGDOIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVYKNDP	184	
Db	122	REVLGNEIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLHCGKSFVYKNDP	181	
Qy	185	FIGVOLGAVKXNVIAGMSDGIQFGANARTALITRGLAEMSRIGALGADPATFMGMA	244	
Db	182	FIGVOLGAVKXNVIAGMSDGIQFGANARTALITRGLAEMSRIGALGADPATFMGMA	241	
Qy	245	GLGDLVLTCTENQSRNRRFGMLGQGMVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEM	304	
Db	242	GLGDLVLTCTENQSRNRRFGMLGQGMVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEM	301	
Qy	305	PITEIYQVLYCKNAREAAALTLGRARKDERSS	338	
Db	302	PITEIYQVLYCKNAREAAALTLGRARKDERSS	335	

Search completed: April 27, 2005, 10:59:44
Job time : 167 secs

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OM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 09:52:56 ; Search time 656 Seconds
(without alignments)
9204.476 Million cell updates/sec

Title: US-10-088-079-1

Perfect score: 1020

Sequence: 1 atgaaccaagctaatgttc.....acgagcgagcagcactaa 1020

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	100.0	1020	5	Aaf57428 E. coli g
2	1018.4	99.8	1020	4	Aas52655 E. coli D
3	1018.4	99.8	1020	8	Aca32689 Prokaryot
4	1018.4	99.8	1020	13	Adt48853 Bacterial
5	787	77.2	1020	8	Aca51335 Prokaryot
6	765.8	75.1	1017	8	Aca31966 Prokaryot
7	756.6	74.2	1017	8	Aca35838 Prokaryot
8	749.4	73.5	1023	11	Ach97774 Klebsiell
9	749.4	73.5	1023	8	Aca49224 Prokaryot
10	606	59.4	1020	8	Aca54019 Prokaryot
11	565.6	55.5	781	6	Abq21987 Oligonucl
12	565.6	55.5	781	6	Abq21986 Oligonucl
13	556.4	54.5	1023	10	Acf70491 Photorhab
14	556.4	54.5	6972	10	Acf65374 Photorhab
15	556.4	54.5	110000	10	Continuation (36 o
16	539.6	52.9	1011	8	Aca44463 Prokaryot
17	539.6	52.9	1023	10	Adf03046 Bacterial
18	539.4	52.9	990	13	Ads45613 Bacterial
19	521.2	51.1	990	13	Adt46572 Bacterial
20	513.8	50.4	781	6	Abq21989 Oligonucl

C	21	513.8	50.4	781	6	Abq21988 Oligonucl
	22	476.2	46.7	1035	8	ACA53490 Prokaryot
	23	414.4	40.5	1014	8	ACA43241 Prokaryot
	24	399.4	39.2	135356	13	ADT05646 Haemophil
	25	396.2	38.8	1008	4	AAS53331 Haemophil
	26	396.2	38.8	1008	8	ACA34182 Prokaryot
	27	396.2	38.8	110000	2	Continuation (7 of
C	28	388.4	38.1	4711	13	ADT05428 Haemophil
	29	325.6	31.9	503	6	Abq50341 Oligonucl
C	30	325.6	31.9	503	6	Abq50340 Oligonucl
	31	313.8	30.8	503	6	Abq50339 Oligonucl
	32	313.8	30.8	503	6	Abq50338 Oligonucl
	33	238.6	23.4	1002	13	ADT41591 Bacterial
	34	238.6	23.4	1002	13	ADS63997 Bacterial
	35	238.6	23.4	1020	13	ADS63622 Bacterial
	36	221	21.7	1041	13	ADT42864 Bacterial
	37	219.4	21.5	987	8	ACA37060 Prokaryot
	38	211.4	20.7	1002	13	ADS57169 Bacterial
	39	199.8	19.6	987	8	Abx09916 N. mening
	40	199.8	19.6	49767	3	AAA81458 N. mening
C	41	199.8	19.6	110000	3	AAA81489 7
C	42	199.8	19.6	110000	4	RAI9682_33
C	43	199.8	19.6	110000	4	RAI9682_33
C	44	199.8	19.6	172325	3	AAF21613 Neisseria
	45	199.6	19.6	1002	8	ACA38486 Prokaryot

ALIGNMENTS

RESULT 1

AAF57428
ID AAF57428 standard; DNA; 1020 BP.

XX AAF57428;

AC AAF57428;

DT 11-JUN-2001 (first entry)

DE E. coli gpsA2FR encoding DNA.

XX Glycerol-3-phosphate dehydrogenase; G3PD; feedback inhibition; oil seed;

KW Genetic transformation; fatty acid; glycerolipid; osmotic stress; gpsA;

KW gpsA2FR; allele; ds.

OS Escherichia coli.

XX Key Location/Qualifiers

FT CDS 1..1020

FT /*tag= a

FT /product= "gpsA2FR"

FT mutation 765

FT /*tag= b

FT /note= "there is a point mutation at this position as

FT compared to the wild-type gpsA gene, which makes the gene

FT feed-defective; wild-type GAC codon is changed to GAA

FT codon"

FT

FT

FT

FT

FT

PT stress tolerance, altering fatty acid content in glycerolipids, by
PT expressing in plant feedback defective glycerol-3-phosphate dehydrogenase
PT gene.
XX
PS
PS
XX

Claim 5; Fig 1; 39pp; English.

XX The invention provides a method for genetically transforming a plant so
CC that it expresses a heterologous glycerol-3-phosphate dehydrogenase
CC (G3PD) that is less sensitive to feedback inhibition than wild-type G3PD.
CC The method involves providing a vector comprising a DNA sequence encoding
CC G3PD that is less sensitive to feedback inhibition than wild-type G3PD
CC and transforming the plant with the vector. The method is useful for
CC expressing a heterologous G3PD less sensitive to feedback inhibition than
CC wild-type G3PD in an oil seed bearing plant, such as Arabidopsis thaliana
CC or Brassica. The vectors are useful for producing a genetically altered
CC plant having altered fatty acid content in its glycerolipids, especially
CC elevated levels of C16 fatty acids and increased osmotic stress tolerance
CC relative to the wild type. The present sequence represents the DNA
CC encoding the E. coli gpa2FR protein. The gene gpa2FR is an allele of
CC the E. coli gpa gene, and encodes an altered version of the GPDH protein
CC defective in feedback inhibition. This gpa2FR gene can be used in the
CC vectors and method of the invention
XX

SQ Sequence 1020 BP; 214 A; 274 C; 304 G; 228 T; 0 U; 0 Other;

Query Match 100.0%; Score 1020; DB 5; Length 1020;
Best Local Similarity 100.0%; Pred. No. 2.1e-308;
Matches 1020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACCAACGTAATGCTTCAATGACGTGATCGGCGCGCTGTACGGCACCCTCTT 60
DB 1 ATGAACCAACGTAATGCTTCAATGACGTGATCGGCGCGCTGTACGGCACCCTCTT 60
QY 61 GCCATCACCTGGCAAGAAATGGCCACGAGTTGCTCTGGGGCCATGACCCCTGAACAT 120
DB 61 GCCATCACCTGGCAAGAAATGGCCACGAGTTGCTCTGGGGCCATGACCCCTGAACAT 120
QY 121 ATGCAACGCTTGAAACGCGGCTGTAAACGCGGTTTCTCCCGATGTGCTTTTCCC 180
DB 121 ATGCAACGCTTGAAACGCGGCTGTAAACGCGGTTTCTCCCGATGTGCTTTTCCC 180
QY 181 GATACGCTCCATCTTGAAGAGGATCTGCCACTCGCTGCGCAGCCGCTAATATTCTC 240
DB 181 GATACGCTCCATCTTGAAGAGGATCTGCCACTCGCTGCGCAGCCGCTAATATTCTC 240
QY 241 GTGCTGTACCCAGCCATGCTTTTGGTGAAGTGTGCGCCAGATTAACCACTGATCGGT 300
DB 241 GTGCTGTACCCAGCCATGCTTTTGGTGAAGTGTGCGCCAGATTAACCACTGATCGGT 300
QY 301 CTTGATCGGCTGTGTTGGGCGACCAAGGGCTGGAAGCGGAAACCGGACGCTCTGTTA 360
DB 301 CTTGATCGGCTGTGTTGGGCGACCAAGGGCTGGAAGCGGAAACCGGACGCTCTGTTA 360
QY 361 CAGGACGTGGCGGTGAGGCTTAGGCGATCAAAATCCGCTGGCGGTTATCTCTGGCCCA 420
DB 361 CAGGACGTGGCGGTGAGGCTTAGGCGATCAAAATCCGCTGGCGGTTATCTCTGGCCCA 420
QY 421 ACGTTTCGGAAGAACTGGCGGCAAGTTTACCGACAGCTATTTTCGCTGGCTCGACCGAT 480
DB 421 ACGTTTCGGAAGAACTGGCGGCAAGTTTACCGACAGCTATTTTCGCTGGCTCGACCGAT 480
QY 481 CAGACCTTTCCGATGATCTCCAGCAGCTGTGACCTGGCGCAAAAGTTTCGCGGTTTAC 540
DB 481 CAGACCTTTCCGATGATCTCCAGCAGCTGTGACCTGGCGCAAAAGTTTCGCGGTTTAC 540
QY 541 AGCAATCCGATTTTCTGGGCTGACGTTGGCGGCGGTTGAAGAACTTATTGCCATT 600
DB 541 AGCAATCCGATTTTCTGGGCTGACGTTGGCGGCGGTTGAAGAACTTATTGCCATT 600
QY 601 GGTGCGGGGATGTCGACGATCGGTTTGGTGGCAATGCGGCTACGGCGCTGATCACC 660
DB 601 GGTGCGGGGATGTCGACGATCGGTTTGGTGGCAATGCGGCTACGGCGCTGATCACC 660

QY 661 CGTGGCGCTGCTGAAATGTCGCGTCTTGGTGGCGGCTGGTGGCGGCTGGCGGCTTTT 720
DB 661 CGTGGCGCTGCTGAAATGTCGCGTCTTGGTGGCGGCTGGTGGCGGCTGGCGGCTTTT 720
QY 721 ATGGGCAATGCGGGGCTTGGCGATCTGGTCTTACCTGTACCGGAAACCACTGCGGTAAC 780
DB 721 ATGGGCAATGCGGGGCTTGGCGATCTGGTCTTACCTGTACCGGAAACCACTGCGGTAAC 780
QY 781 CGCGGTTTGGCAATGATGCTGCGGTGAGGCGATGATGATCAAAAGCGGAGGAGATT 840
DB 781 CGCGGTTTGGCAATGATGCTGCGGTGAGGCGATGATGATCAAAAGCGGAGGAGATT 840
QY 841 GGTGAGTGTGGAAGGCTTACCGATACCAAGAGTCCGCACTGGCGGCTGCTTC 900
DB 841 GGTGAGTGTGGAAGGCTTACCGATACCAAGAGTCCGCACTGGCGGCTGCTTC 900
QY 901 GGGCTTGAATGCCAATTAACCGAGGAAATTTATCAAGTATTATATTCGGAAAAACGCG 960
DB 901 GGGCTTGAATGCCAATTAACCGAGGAAATTTATCAAGTATTATATTCGGAAAAACGCG 960
QY 961 CGCGAGGCGACATGACTTTTACTAGTCTGTCGACGCAAGGAGCGAGCGGCGGCTTAA 1020
DB 961 CGCGAGGCGACATGACTTTTACTAGTCTGTCGACGCAAGGAGCGAGCGGCGGCTTAA 1020

RESULT 2
AAS52655

ID AAS52655 standard; DNA; 1020 BP.

XX AAS52655;

XX 13-FEB-2002 (first entry)

XX E. coli DNA for cellular proliferation protein #377.

XX Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;

XX antibacterial; drug design.

XX Escherichia coli.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US0009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX P-PSDB; AAU34796.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids.

XX Claim 27; SEQ ID NO 6292; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

XX prokaryotic cellular proliferation, their use in identifying the genes,

XX their use in the discovery of novel antibiotics, the essential genes

XX themselves and the encoded proteins. The prokaryotes used are Escherichia

XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,

XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Query Match 99.8%; Score 1018.4; DB 4; Length 1020;

Best Local Similarity 99.9%; Pred. No. 6.8e-308;

Matches 1019; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCGGCTCGTACGGCACCCTCTT	60
Db	1	ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCGGCTCGTACGGCACCCTCTT	60
Qy	61	GCCATACCCCTGGCAAGAAATGGCGACGAGTTGCTCTGGGGCCATGACCCCTGAACAT	120
Db	61	GCCATACCCCTGGCAAGAAATGGCGACGAGTTGCTCTGGGGCCATGACCCCTGAACAT	120
Qy	121	ATCGCAACGCTTGAAACGGACCGCTGTAACGCGGTTTCTCCCGATGTCCTTTTCCC	180
Db	121	ATCGCAACGCTTGAAACGGACCGCTGTAACGCGGTTTCTCCCGATGTCCTTTTCCC	180
Qy	181	GATACGCTCCATCTTTGAAAGGATCTCGCCACTCGCTGGCAGCAGCGTAATATCTC	240
Db	181	GATACGCTCCATCTTTGAAAGGATCTCGCCACTCGCTGGCAGCAGCGTAATATCTC	240
Qy	241	GTGCTGTACCCAGCCATGCTTTTGGTGAAGTGTGCGCCAGATTAACCACTGATCGT	300
Db	241	GTGCTGTACCCAGCCATGCTTTTGGTGAAGTGTGCGCCAGATTAACCACTGATCGT	300
Qy	301	CCTGATCGGCTGTGTTGGGACCAACAAAGGGCTGGAGGGGACCGGACGCTCTGTA	360
Db	301	CCTGATCGGCTGTGTTGGGACCAACAAAGGGCTGGAGGGGACCGGACGCTCTGTA	360
Qy	361	CAGACGCTGGCGCTGAGGCTTACGAGGATCAAAATTCGCTGGCGGTTATCTCGGCCA	420
Db	361	CAGACGCTGGCGCTGAGGCTTACGAGGATCAAAATTCGCTGGCGGTTATCTCGGCCA	420
Qy	421	ACGTTTGCAGAAAGAACTGGCGGAGGTTTACCGACAGCTATTTGCTGGCCTCGACCGAT	480
Db	421	ACGTTTGCAGAAAGAACTGGCGGAGGTTTACCGACAGCTATTTGCTGGCCTCGACCGAT	480
Qy	481	CAGACCTTTGCGGATGATCTCAGCAGCTGCTGCACTGCGCAAAAGTTTCGGGTTAC	540
Db	481	CAGACCTTTGCGGATGATCTCAGCAGCTGCTGCACTGCGCAAAAGTTTCGGGTTAC	540
Qy	541	AGCAATCCGATTTTCATTGGGCTGCGCTGGCGCGCGTGAAGAAAGTTTATTCGCATT	600
Db	541	AGCAATCCGATTTTCATTGGGCTGCGCTGGCGCGCGTGAAGAAAGTTTATTCGCATT	600
Qy	601	GGTCGGGGATGTCGACGGTATCGTTTGGTGGCAATGCGGTACGGGCTGATCAAC	660
Db	601	GGTCGGGGATGTCGACGGTATCGTTTGGTGGCAATGCGGTACGGGCTGATCAAC	660
Qy	661	CGTGGCTGGCTGAATGTCGCTTGGTGGCGGCTGGGTGCGGACCTTCCACCTTT	720
Db	661	CGTGGCTGGCTGAATGTCGCTTGGTGGCGGCTGGGTGCGGACCTTCCACCTTT	720
Qy	721	ATGGCATGGCGGGCTTGGCGATCTGGTCTTACCTGTACCGAAACAGTCGCGTAAC	780
Db	721	ATGGCATGGCGGGCTTGGCGATCTGGTCTTACCTGTACCGAAACAGTCGCGTAAC	780
Qy	781	CGCGCTTTGTCATGCTCGGTGAGGGCATGATGTACAAAGCGCGCAGGAGGAT	840
Db	781	CGCGCTTTGTCATGCTCGGTGAGGGCATGATGTACAAAGCGCGCAGGAGGAT	840

Db	781	CGCGCTTTGTCATGCTCGGTGAGGGCATGATGTACAAAGCGCGCAGGAGGAT	840
Qy	841	GGTCAGGTGGTGAAGCTACCGCAATACGAAAGTCCGCAACTGGCGCATCGCTTC	900
Db	841	GGTCAGGTGGTGAAGCTACCGCAATACGAAAGTCCGCAACTGGCGCATCGCTTC	900
Qy	901	GGCCTTGAATGCCAATAACCGAGAAATTTATCAAGTATTATTTGCGGAAAAACCGG	960
Db	901	GGCCTTGAATGCCAATAACCGAGAAATTTATCAAGTATTATTTGCGGAAAAACCGG	960
Qy	961	CGCGAGGAGCATGACTTTACTAGGTCGTCACGCAAGGAGGAGCGCAGGCACTAA	1020
Db	961	CGCGAGGAGCATGACTTTACTAGGTCGTCACGCAAGGAGGAGCGCAGGCACTAA	1020

RESULT 3

ACA32689

ID ACA32689 standard; DNA; 1020 BP.

XX ACA32689;

XX AC AC

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #14346.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX Escherichia coli.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-PSDB; ABU28819.

XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 20559; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The present sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Query Match 99.8%; Score 1018.4; DB 8; Length 1020;
Best Local Similarity 99.9%; Pred. No. 6.8e-308;
Matches 1019; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCGGCTCGTACGGCACCCTCTTT 60
Db 1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCGGCTCGTACGGCACCCTCTTT 60
Qy 61 GCCATCACTCCCTGGCAAGAAATGGCCACGAGTTTGTCTCTGGGGCCATGACCCCTGAACAT 120
Db 61 GCCATCACTCCCTGGCAAGAAATGGCCACGAGTTTGTCTCTGGGGCCATGACCCCTGAACAT 120
Qy 121 ATCGCAACGCTTGAACCGACCGCTGTAAACGCGCTTCTCCCGATGCGCTTTTCCC 180
Db 121 ATCGCAACGCTTGAACCGACCGCTGTAAACGCGCTTCTCCCGATGCGCTTTTCCC 180
Qy 181 GATACGCTCCATCTPTGAAAGCGATCTGCCACTCGCTGCGCAGCGCGTAAATATCTC 240
Db 181 GATACGCTCCATCTPTGAAAGCGATCTGCCACTCGCTGCGCAGCGCGTAAATATCTC 240
Qy 241 GTCTGTGTACCCAGCATGCTTTGGTGAAGTGTGCTGCCAGATTAACCACTGATCGGT 300
Db 241 GTCTGTGTACCCAGCATGCTTTGGTGAAGTGTGCTGCCAGATTAACCACTGATCGGT 300
Qy 301 CCTGATCGGCTGTGTTGGCGCACCAAGGGCTGGAAGCGGAAACCGGACGCTCTGTA 360
Db 301 CCTGATCGGCTGTGTTGGCGCACCAAGGGCTGGAAGCGGAAACCGGACGCTCTGTA 360
Qy 361 CAGGACGTGGCGGTGAGGCTTATAGGCGATCAAAATCCGCTGGCGGTATCTCTGGCCCA 420
Db 361 CAGGACGTGGCGGTGAGGCTTATAGGCGATCAAAATCCGCTGGCGGTATCTCTGGCCCA 420
Qy 421 ACGTTTGGAAAGAACTGGCGGAGGTTTACCGACAGCTATTTGCTGGCTCGACCGAT 480
Db 421 ACGTTTGGAAAGAACTGGCGGAGGTTTACCGACAGCTATTTGCTGGCTCGACCGAT 480
Qy 481 CAGACCTTTGCGATGATCTCCACAGCTGCTGCACTGCGCAAAAGTTTCCGGTATTAC 540
Db 481 CAGACCTTTGCGATGATCTCCACAGCTGCTGCACTGCGCAAAAGTTTCCGGTATTAC 540
Qy 541 AGCAATCCGATTTTCAATGGCGTACGCTTGGCGGCGGCTGGAACAGTTTATGGCAAT 600
Db 541 AGCAATCCGATTTTCAATGGCGTACGCTTGGCGGCGGCTGGAACAGTTTATGGCAAT 600
Qy 601 GGTGCGGGATGTCGAGCGTATCGGTTTGGTGGCAATGCGGTACGGGCTGATCACC 660
Db 601 GGTGCGGGATGTCGAGCGTATCGGTTTGGTGGCAATGCGGTACGGGCTGATCACC 660
Qy 661 CGTGGGCTGGCTGAAATGTCGCTTGGTGGCGGCTGGGTGCGGACCTTGCACCTTT 720
Db 661 CGTGGGCTGGCTGAAATGTCGCTTGGTGGCGGCTGGGTGCGGACCTTGCACCTTT 720
Qy 721 ATGGGCATGCGGGCTTGGCGATCTGGTGTATCTACCTGTATCCGAAAAACAGTCCGCTAAC 780
Db 721 ATGGGCATGCGGGCTTGGCGATCTGGTGTATCTACCTGTATCCGAAAAACAGTCCGCTAAC 780

Qy 781 CGCGGTTTTGGCATGATGCTCGGTACGGGATGATGATCAAAAGCGCGCAGGAGATT 840
Db 781 CGCGGTTTTGGCATGATGCTCGGTACGGGATGATGATCAAAAGCGCGCAGGAGATT 840
Qy 841 GGTCAAGTGTGGAAGGCTACCGCAATACGAAAGAGTCCGGAACCTGGCGCATCGCTTC 900
Db 841 GGTCAAGTGTGGAAGGCTACCGCAATACGAAAGAGTCCGGAACCTGGCGCATCGCTTC 900
Qy 901 GCGGTTGAAATGCAATAAACCGAGGAAATTTATCAAGTATTTATATTCGGAAAAACGCG 960
Db 901 GCGGTTGAAATGCAATAAACCGAGGAAATTTATCAAGTATTTATATTCGGAAAAACGCG 960
Qy 961 CGCGAGGACGATGATCTTTACTAGTGTGCGCAGGCAAGACGCGCAGGACCACTAA 1020
Db 961 CGCGAGGACGATGATCTTTACTAGTGTGCGCAGGCAAGACGCGCAGGACCACTAA 1020
RESULT 4
ADT48853
ID ADT48853 standard; cDNA; 1020 BP.
XX
AC ADT48853;
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #23604.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2002333675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 47291; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX

SQ Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Query Match 99.8%; Score 1018.4; DB 13; Length 1020;
 Best Local Similarity 99.9%; Pred. No. 6.8e-308;
 Matches 1019; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCGGCTGTACGGCACCGCTCTT 60
 Db 1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCGGCTGTACGGCACCGCTCTT 60

Qy 61 GCCATCACCTGGCAAGAAATGCGCACGAGGTGTCTCTGGGGCCATGACCTGAACAT 120
 Db 61 GCCATCACCTGGCAAGAAATGCGCACGAGGTGTCTCTGGGGCCATGACCTGAACAT 120

Qy 121 ATCGCAACGCTTGAACGCGCGCTGTAAACCGCGGTTCTCCCGATGTCCTTTCCC 180
 Db 121 ATCGCAACGCTTGAACGCGCGCTGTAAACCGCGGTTCTCCCGATGTCCTTTCCC 180

Qy 181 GATACGCTCCATCTTGAAGCGATCTCGCCACTGCGCTGGCAGCGCGTAATATCTC 240
 Db 181 GATACGCTCCATCTTGAAGCGATCTCGCCACTGCGCTGGCAGCGCGTAATATCTC 240

Qy 241 GTGCTGTACCCAGCCATGTCTTTGGTGAAGTGTGCGCCAGATTAACACCTGATGCGT 300
 Db 241 GTGCTGTACCCAGCCATGTCTTTGGTGAAGTGTGCGCCAGATTAACACCTGATGCGT 300

Qy 301 CCTGATCGGCTCTGCTGGCGCACCAAGGGCTGGAAGCGGAACCGGACGCTCTGTTA 360
 Db 301 CCTGATCGGCTCTGCTGGCGCACCAAGGGCTGGAAGCGGAACCGGACGCTCTGTTA 360

Qy 361 CAGACGCTGGCGCGCTGAGCGCTTAGCGCATCAATTCGCGTGGCGGTATCTCTGGCCCA 420
 Db 361 CAGACGCTGGCGCGCTGAGCGCTTAGCGCATCAATTCGCGTGGCGGTATCTCTGGCCCA 420

Qy 421 ACGTTTGCAGAAAGAACTGGCGCAGGTTTACCGACAGCTATTTGCTGGCTCGACCGAT 480
 Db 421 ACGTTTGCAGAAAGAACTGGCGCAGGTTTACCGACAGCTATTTGCTGGCTCGACCGAT 480

Qy 481 CAGACCTTTGCGGATGATCTCAGCAGCTGCTGCACTGCGGCAAAAGTTTCGGGTTTAC 540
 Db 481 CAGACCTTTGCGGATGATCTCAGCAGCTGCTGCACTGCGGCAAAAGTTTCGGGTTTAC 540

Qy 541 AGCAATCCGATTTTCATTTGGGCTGCGAGCTTGGCGCGGCTGAAACGTTATTGCCATT 600
 Db 541 AGCAATCCGATTTTCATTTGGGCTGCGAGCTTGGCGCGGCTGAAACGTTATTGCCATT 600

Qy 601 GGTGGGGGATGTCCGACGGTATCGGTTTGGTGGCAATGCGCGTACGGCGCTGATCAC 660
 Db 601 GGTGGGGGATGTCCGACGGTATCGGTTTGGTGGCAATGCGCGTACGGCGCTGATCAC 660

Qy 661 CGTGGGCTGGCTGAATTCGGGCTTGGTGGCGGCTGGGTGCGGACCTGCCACCTTT 720
 Db 661 CGTGGGCTGGCTGAATTCGGGCTTGGTGGCGGCTGGGTGCGGACCTGCCACCTTT 720

Qy 721 ATGGCATGGCGGGCTTGGCGATCTGCTGTACTCTGACGAAACCAAGTGGGTAAC 780
 Db 721 ATGGCATGGCGGGCTTGGCGATCTGCTGTACTCTGACGAAACCAAGTGGGTAAC 780

Qy 781 CGCCGTTTGGCATGATGCTCGGTGAGGCGATGATGTACAAAGCGCGCAGGAGAAGATT 840
 Db 781 CGCCGTTTGGCATGATGCTCGGTGAGGCGATGATGTACAAAGCGCGCAGGAGAAGATT 840

Db 781 CGCCGTTTGGCATGATGCTCGGTGAGGCGATGATGTACAAAGCGCGCAGGAGAAGATT 840
 Qy 841 GGTGAGGTGGTGGAGGCTACCGCAATACGAAAGAGTCCGGAAGTCCGCACTGCGCATCGCTTC 900
 Db 841 GGTGAGGTGGTGGAGGCTACCGCAATACGAAAGAGTCCGGAAGTCCGCACTGCGCATCGCTTC 900
 Qy 901 GGCCTTGAATGCGCAATTAACCGCAGGAAATTTATCAAGTATTATTTGCGGAAAAACCGG 960
 Db 901 GGCCTTGAATGCGCAATTAACCGCAGGAAATTTATCAAGTATTATTTGCGGAAAAACCGG 960
 Qy 961 GCGCAGGCGAGCATTTGACTTTTACTAGTCTGCGCAGGAGGAGCGCAGGAGCCACTAA 1020
 Db 961 GCGCAGGCGAGCATTTGACTTTTACTAGTCTGCGCAGGAGGAGCGCAGGAGCCACTAA 1020

RESULT 5
 ACAS1335
 ID ACAS1335 standard; DNA; 1020 BP.
 XX ACA51335;
 AC ACA51335;
 DT 19-JUN-2003 (first entry)
 XX Prokaryotic essential gene #32992.
 DE Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX Salmomella typhi.
 OS WO200277183-A2.
 PN 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 PF 21-MAR-2002; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR P-PSDB; ABU47465.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 14; SEQ ID NO 39205; 1766bp; English.
 PS The invention relates to an isolated nucleic acid comprising any one of
 CC the 613 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 1017 BP; 207 A; 289 C; 312 G; 209 T; 0 U; 0 Other;

Query Match		75.1%	Score 765.8;	DB 8;	Length 1017;
Best Local Similarity		84.6%	Pred. No. 8.6e-229;		
Matches		860;	Conservative	0;	Mismatches 157; Indels 0; Gaps 0;
Qy	1	ATGAACCAACGTAATGCTTCAATGATCTGATCGTGGCGCTGATCGGCACCGCTCTT	60		
Db	1	ATGAGCACTGTTAATGCGTCAATGACTGTGATCGTGGCGCTCATACGGCACCGCTCTT	60		
Qy	61	GCCATCACTCCCTGGCAAGAAATGGCCACGAGGTTGCTCTCGGGCCATGACCCGTAACAT	120		
Db	61	GCCATCACTCCCTGGCAAGAAATGGTACGAAGTGTCTCTGGGGCCACGACCCAAAACAT	120		
Qy	121	ATCGCAACGCTTGTAACGCGACCGCTGTAAACGCGGTTTCTCCCGATGTGCTTTTCCC	180		
Db	121	ATCGCAACGCTTGTAACGCGACCGTTGTAAAGTGGGTTTCTTCCGGAGTTTCCGTTCCC	180		
Qy	181	GATACGCTCATCTTTGAAGCGATCTCCGACTGCGCTGGCAGCGCGTAATATCTC	240		
Db	181	GACTCCCTGCACTTTGAAGGCGACCTTGCACCGCGCTGGCGGCGCAGCGCAACATCTG	240		
Qy	241	GTCGTGCTGACCCAGCCATGCTTTGGTGAAGTGTGCGCCAGATTAAACCACTGATGGT	300		
Db	241	ATTGTGTTTCGAGCCATGATTTTGGCAGCTGCTCCGTCAGATTAAACCCGCTGATGGC	300		
Qy	301	CCTGATCGCGCTCTGGTGTGGCGCACCAAGAGGCTGGAAGCGGAAACCGGACGCTCTTTA	360		
Db	301	CCGATGCGCGCATTTGCTGGCGGACAAAGGACTGGAAGCGGAAACCGGACGCTCTG	360		
Qy	361	CAGGACGTGGCGGCTGAGCGCTTAGCGATCAAAATTCGCTGGCGGTATCTTGCGCCA	420		
Db	361	CAGGACGTGGCGGCGAAGCGCTGGGTGATGCGATCCCGCTGGCGGTATCTCGGCGCG	420		
Qy	421	ACGTTTGGGAAGAACTGGCGGCGAGTTTACCGACAGCTATTTCGTCGGCTCGACCGAT	480		
Db	421	ACCTTTGCCAAGAGCTGGCGCTGGCTGCGGCGGATTCGCTGGCTCCACCGAT	480		
Qy	481	CAGACCTTTGCGGATGATCTCAGCAGCTGCTGCACTCGCGCAAAAGTTTCCGGTTTAC	540		
Db	481	CAGGCTTTCTCGAGCATTTCAACAGCTGCTGCACTCGCGCAAGAGCTTCGCGTCTAC	540		
Qy	541	AGCAATCCGATTTTCATTGGGTGCGAGCTTGGCGGCGCGGTGAAACGTTATTGCCATT	600		
Db	541	AGCAATCCGATTTTATCGGCTGCACTGGCGGCGGTGCGGTGAAGAACGTTATTGCCATT	600		
Qy	601	GTCGCGGAGTGTCCGAGGATCGGTTTTCGTCGATGCGGTGCGGCTGATCAC	660		
Db	601	GGCGCGGAGTGTACAGCGCATTTGTTTGTGCAATGCGGTACGGCGCTGATCAC	660		
Qy	661	CGTGGCTGCGTGAATGCTCGGCTCTGGTGGCGGCTGGGTGCGGACCCCTGCCACCTTT	720		
Db	661	CGAGGCTAACCGAAATGCTCCGCTGGCGAAGCGCTGGGTGCGGATCCGGCCACCTTT	720		
Qy	721	ATGGGATGCGGCGCTGGCGATCTGGTCTTACCGGAAACCAAGTCGCGTAAC	780		

Db	721	ATGGGAATGCTGGCTGGCGGACCTGGTCTGCTACCGATAACCAAGTCCTCGTAAC	780
Qy	781	CGCGTCTTTGGCATGCTCGTCCAGGCATGATGTACAAGCGCGCAGGAGATTT	840
Db	781	CGCGTCTTTGGCATGATGCTCGGACAGGCGAGCATGTTAAAGGCGCGCAGGAGATTT	840
Qy	841	GCTCAGGTGGTGAAGGCTACCGCAATACGAAAGTCCGCGAACTCGCGCATCGCTTC	900
Db	841	GCTCAGGTGGTGAAGGCTACCGCAATACGAAAGTCCGCGAGTTGCGCGCACCGTTTC	900
Qy	901	GGCTTGAATGCCAATAACCGAGAAATTTATCAAGTATTATTTGGGAAAAAACCGG	960
Db	901	GGTGTGGAATGCCAATAACCGAGAAATTTATCAGGTATTGTATTGGGAAAAAATCG	960
Qy	961	CGCGAGGCGAGCATTTGACTTTTACTAGTCTGTCGCAAGGACGCGCAGCGCCAC	1017
Db	961	CGCGAGGCGAGCATTTGACCTTTATTAGTCTGTCGCGCAAGGACGCGCAGCGATTAAC	1017

RESULT 7
ACA35838

ID ACA35838 standard; DNA; 1017 BP.

XX ACA35838;

DT 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #17495.

XX Antisense; db; prokaryotic essential gene; cell proliferation;
XX drug design; gene.

OS Klebsiella pneumoniae.

XX WO200277183-A2.

PD 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-PSDB; ABU31968.

XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.

PS Claim 14; SEQ ID NO 23708; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1017 BP; 194 A; 306 C; 319 G; 198 T; 0 U; 0 Other;

Query Match 74.2%; Score 756.8; DB 8; Length 1017;
 Best Local Similarity 84.1%; Pred. No. 5.7e-226;
 Matches 854; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

Qy 1 ATGAACCAAGTAAATGCTTCAATGACTGTGATGCTGCGGCTGCTGACCGACCGCTCTT 60
 Db 1 ATGAACGACCTTAATGCTGCAATGACTGTGATGCTGCGGCTGCTTACCGACCGCTCTT 60

Qy 61 GCCATACCCCTGGCAAGAAATGGCCAGAGTCTCTCTGGGGCCATGACCTGGAACAT 120
 Db 61 GCCATACCCCTGGCAAGAAATGGCCAGAGTCTCTCTGGGGCCATGACCCGAAACAT 120

Qy 121 ATCCGAACGCTTGAACGCGACCGCTGTAAACGCCGCTTTCTCCCGATGTGCTTTTCCC 180
 Db 121 ATCCGCGAGCTGCAACAGCATGCTGTCAACGCCGCTTTCTTCCCGATGTGCTTTCCCG 180

Qy 181 GATAGCTTCATCTTGAAGGATCTGCCACTGCGCTGGAGCCAGCGGTATATATCTC 240
 Db 181 GATAGCTGTCATCTTGAGAGGACCTGGCCACCGCTGCGCGCCAGCGGACATCTT 240

Qy 241 GTCTGTGTACCCAGCCATGCTTTGGTGAAGTGTGCGCCAGATTAACCACTGATCGT 300
 Db 241 GTCTGTGTCCGAGCCATGATTCGGTCAGGTGTACGCCAGATTAACCGCTGATCGT 300

Qy 301 CCTGATCGCGTCTGTGTGGGCAACCAAGGGCTGGAAGCGGAAACCGGACGCTCTGTTA 360
 Db 301 TCCGACGCGGCTGTGTGGGCAACCAAGGGCTTGAGGCCGAAACCGGCGCTCTGCTG 360

Qy 361 CAGGACGTGGCGCTGAGGCGCTTAGGGGATCAAAATTCGCTGGCGGTATCTTGGGCCCA 420
 Db 361 CAGGACGTGGCGCTGAGGCGCTTAGGGGATGATATTCGCTGGCGGTGATCTCGGGGCCA 420

Qy 421 ACCTTTCGAAGAACTGGGCGGAGTTTACGACAGCTATTTCCGCTGGCTCGACCGAT 480
 Db 421 ACCTTTCGAAGAACTGGGCGGAGTTTACGACAGCGGATTTCCGCTGGCGGCGACCGAT 480

Qy 481 CAGACCTTTGCGGATGATCTTCAGCAGTGTGCTGCTGCGGCAAAAGTTTCCGCGTTTAC 540
 Db 481 CCGCAGTTTGGGAGGACCTTTCAGCGCTACTGCTGCTGCGGCAAAAGTTTCCGCGTCTAC 540

Qy 541 AGCAATCCGATTTTCATTTGGGTGCGCTGCGGCGGCGGTGAAACGTTATTTGCCATT 600
 Db 541 ATCAACCCGACTTTATTCGGGCTGCGCTGCGGCGGCGGTGAAACGTTATTTGCCATC 600

Qy 601 GGTGCGGAGTGTCCGAGCGGTATCGGTTTGGTGGCAATGCGGTACGGCGCTGATCAC 660
 Db 601 GGGGAGGATGTTCGAGCGGATCGGTTTGGCGCCAAATGCGGTACGGCGCTGATTTACC 660

Qy 661 CGTGGGCTGGTGAATGTTCGCGTCTTTGGTGGCGGCTGGGTGCGGACCTTGCACCTTT 720
 Db 661 CGTGGGCTGGTGAATGTTCGCGCTCGGCGCGGCTGGGCGCGGATTCGCGAACCTTT 720

Qy 721 ATGGGATGCGGGGCTTGGCGATCTGGTCTTACCTGTACCGAAGAACCGTCCGCTAAC 780
 Db 721 ATGGGATGCGGGGCTTGGCGATCTGGTCTTACCTGTACCGAAGAACCGTCCGCTAAC 780

Qy 781 CGCGTTTGGCATGATGCTCGGTTCAGGCGATGATGATCAAAAGCGCGCAGGAGAAATT 840
 Db 781 CGTGGCTTGGCATGATGCTCGGCGAGGTATGAGCGTGCAGAGCGCCAGGACAAATT 840

Qy 841 GGTGAGTGTGGAAGCTTACCGCAATACGAAAGAAAGTCCGCGAACTGGCGCATCGCTTC 900
 Db 841 GGCAGGTGTGGAAGCTTACCGCAATACGAAAGAAAGTCCGCGTTCTGGCACAGCGTTTA 900

Qy 901 GCGTTGAAATGCAATAACCGAGGAAATTTATCAAGTATATATTTGCGGAAAAACGCG 960
 Db 901 GGTGTGAAATGCAATAACCGAGGAAATTTATCAAGTATATTTGCGGAAAAATTTGCG 960

Qy 961 CGCGAGGCGACATTTGACTTTACTAGGTCTGTGCGCAAGGACGAGCGCGCAGCGCA 1016
 Db 961 CGCGAGGCGACATTTGACTTTACTAGGTCTGTGCGCGCGCGGCGAGCGCGCAGCGCA 1016

RESULT 8
 ACH97774
 ID ACH97774 standard; DNA, 1038 BP.
 XX ACH97774;
 AC ACH97774;
 XX 29-JUL-2004 (first entry)
 XX Klebsiella pneumoniae polynucleotide seqid 3569.
 DE Klebsiella pneumoniae polynucleotide seqid 3569.
 XX Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; vaccine; gene; db.
 XX Klebsiella pneumoniae.
 OS Klebsiella pneumoniae.
 XX US6610836-B1.
 XX 26-AUG-2003.
 PD 27-JAN-2000; 2000US-00489039.
 PF 29-JAN-1999; 99US-0117747P.
 PR (GENO-) GENOME THERAPEUTICS CORP.
 XX Breton GL, Osborne M;
 PI WPI; 2003-895346/82.
 DR P-FSDB; ABO64223.
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX Disclosure; SEQ ID NO 3569; 932pp; English.
 PS The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This sequence encodes a Klebsiella
 CC pneumoniae polypeptide of the invention
 XX
 SQ Sequence 1038 BP; 201 A; 310 C; 324 G; 203 T; 0 U; 0 Other;

Query Match 74.2%; Score 756.6; DB 11; Length 1038;
 Best Local Similarity 83.9%; Pred. No. 6.6e-226;
 Matches 855; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 1 ATGAACCAAGTAAATGCTTCAATGACTGTGATGCTGCGGCTGCTGACCGACCGCTCTT 60
 Db 19 ATGAACGACCTTAATGCTGCAATGACTGTGATGCTGCGGCTGCTTACCGACCGCTCTT 78

Qy	61	GCATCACCTGGCAGAAATGGCCACGAGGTGTCTCTGGGGCCATGACCTGAAACAT	120
Db	79	GCCATCACCTGGCAGAAATGGCCACCAACGTTGTCTGTGGGGCCATGACCGAAACAT	138
Qy	121	ATCGCAACGCTTGAACGCGACCGCTGTAAACCGCGGTTTCTCCCGCATGTGCTTTTCCC	180
Db	139	ATCGGACGCTGCAACACGATCGCTGCAACCGCGGTCTCTTCCCGATGTGCTTTCCCG	198
Qy	181	GATACGCTCCATCTTTGAAAGCGATCTCGCCACTGGCTGGCAGCAGCGTAATATTCTC	240
Db	199	GATACGCTGCATCTTGAGAGCGACCTGGCCACCGCGCTGGCGCCAGCCGCGACATCTT	258
Qy	241	GTCGTGTAACCAAGCCATGTCTTTGGTGAAGTGTGCGCCAGATTAACCACTGATGGT	300
Db	259	GTCGTGTGTGCGAGCCATGTATTCTGCTCAGGTGTTACGCCAGATTAAACCGCTGATGGT	318
Qy	301	CTGATGCGCGTCTGGTGTGGCGACCAAGGGCTGGAAGCGGAACCGGACGTCGTGTTA	360
Db	319	TCCACGCGCGGCTGGTGTGGGCCACCAAGGCCCTTGAGGCGCAACCGCGCGCTGCTGTG	378
Qy	361	CAGACGCTGGCGCTGAGCGCTTTAGCGCATCAAAATTCGCTGGCGGTTATCTCTGGCCCA	420
Db	379	CAGACGCTGGCGGTGAAGCGCTGGGCGATGATATTCCGTGGCCGATGATCTCGGGGCCA	438
Qy	421	ACGTTTGCAGAAAGAACTGCGCGCAGGTTTACCGACAGCTATTTCTGCTGGCCTCGACCCGAT	480
Db	439	ACCTTGCAGAAAGACTGGCGCGCGCTGCGCAGCGCGATTTCTGCTGGCGGCCACGGAT	498
Qy	481	CAGACCTTTGCCGATGATCTCCAGACGTCTGTGCACTGGCGGCAAAAGTTTTCGCGGTTTAC	540
Db	499	CCGCAGTTTGGCGAGGACCTTTCAGCGCCTACTGTCACTGCGCAAAAGCTTCGCGCTCTAC	558
Qy	541	AGCAATCCGATTTTCAATTGGCGGTGCAGCTTGGCGGCGCGGTGAAAAAGTTATTGCCATT	600
Db	559	ATCAACCCGCACTTTATCGGCGTGCAGCTCGCGCGCGCGGTGAAAAAGTCATATGCCCATC	618
Qy	601	GGTCGGGCGATGTCGACGGTATCGGTTTGGTGGCAATGCGCTGCAATGCGCTGATCACC	660
Db	619	GGGCGAGGTATGTCCGATGGCATCGGCTTGGCGGCCAATCCGCTACGCGCTGATTACC	678
Qy	661	CGTGGGCTGGCTGAAATGTCGCTCTGGTGGCGCGCTGGGTGCGGACCCCTTGCCACCTTT	720
Db	679	CGTGGGCTGGTGGAAAATGTCGCGCTCGCGCGCGCTGGGCGCCGATCCGGAACCTTT	738
Qy	721	ATGGGCATGGCGGGCTTGGCGATCTGTGCTTACTGTACCGAAAAACAGTCGCGGTAAAC	780
Db	739	ATGGGCATGGCGGCGCTCGGTGACCTGTGTCTCACTGCACCGCAACCGATCCCGTAAAC	798
Qy	781	CGCGCTTTGGCATGATGCTCGGTCAAGGCATGGATGTACAAGCGCGCAGAGAGATT	840
Db	799	CGTGCCTTCGGCATGATGCTCGGCCAGGGTATGGACGTGCAAGAGCGCCCGAGCAAGATT	858
Qy	841	GGTCAGGTGGTGAAGGCTCACCGCAATACGAAAGAAATCCCGGAATCGCGCATCGCTTC	900
Db	859	GGCCAGGTGGTGAAGGCTACCGCAATACCAAGGAAGTTCCGCTTCTGGCACAGGCTTTA	918
Qy	901	GGCGTTGAAATGCCAAATACCGAGGAAATTTATCAAAGTATTATATTGGGGAATAACCGG	960
Db	919	GGTGTGAAATGCCCAATAAACCGAGGAAATTTATCAGGTATTGTTATTCGGAAAAATTCG	978
Qy	961	CGCAGGCGAGCATTTGACTTTTACTAGGTCTGTGCAACCAAGAGCAGCGCAGCAGCACTA	1019
Db	979	CGCAGGCGAGCATTTGACTTTATTTGGGTTCGCGCCCGCAAGGACGACGCGCAGCAGCAATTA	1037

Prokaryotic essential gene #30881.
Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

XX SQ Sequence 1023 BP; 219 A; 272 C; 313 G; 219 T; 0 U; 0 Other;
 Query Match 73.5%; Score 749.4; DB 8; Length 1023;
 Best Local Similarity .85.4%; Pred. NO. 1.2e-223;
 Matches 870; Conservative 0; Mismatches 146; Indels 3; Gaps 3;
 QY 1 ATGAAGCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGCCACCGCTCTT 60

||||| 1 ATGAACAAAGTAATCGTCAATACAGTATCGTGGCGCTCGTACGGCACC-CTCTC 59
61 GCCATACCCCTGGCAAGAAATGGCCACAGAGTTCTCTCTGGGGCCATGACCCCTGGAACAT 120
60 GCCATCACTCTGGCGAAGACGGCCACAGGTTGTCTGTGGGGCCACAGACCCCAAAACAT 119
121 ATGCAACGCTTGAAACCGGACCGGTGTAAAGCGCGCTTTCTCCCGATGTGCTTTTCCC 180
120 ATGCGACCCCTGGAGCAGCATCGTGCACAGTCGCTTCTTCCCGATGTGCTTTTCCC 179
181 GATACGCTCCATCTTGAAGAGCATCTCCGACATCGCTGCGACGACCGCTATATTTCTC 240
180 GATACGTTTACCTTGAAGAGGACATTAGCAACCGCTGCGGCGCATGCTGTAACTCTG 239
241 GTGCTGTACCCAGCCATGCTTTGGTGAAGTGTGCGCCAGATTAAACCACTGATCGT 300
240 GTGTGTGTCCAGCCATGTTTTCAGCGACGTGCTGCGGCGAGATTAAACCGCTGATCGT 299
301 CTGATCGCGCTCTGTGTGGGCGACCAAAAGGGCTGGAAGCGGAAACCGGACGTCCTTTA 360
300 CCGATCGCGCTCTGTGTATGGGCGACCAAAAGGGCTGGAAGCGGAAACCGGCGCGCTGTG 359
361 CAGGACGTGCGGTGAGGCTTAGGCGATCAATTCGGCTGCGGCTTCTCTGGGCCA 420
360 CAGGATGTGCTGCGAAGCGTTAGGCGATCAATCCCGTGGCGGTGATTTCTGGGCCG 419
421 ACGTTTCGGAAGAACTGGCGGCGAGTTTACCGACAGTATTTCTGCTGGCTGCGACGAT 480
420 ACGTTTCGTAAGAAATGGCGGCGGTTT-CGACGCGCAATCTCTGGCTCAACCGAT 478
481 CAGACCTTTGCGGATGATCTCAGCAGCTGTGCACTGCGGCGAAGTTTTCGCGTTTAC 540
479 GAGACCTTTGCGGACGATCTCCAGCAACTGTGCACTGCGGCGAAGTTTTCGCGCTAT 538
541 AGCAATCGGATTTCAATTGGCTGCGCTGGCGCGCGGTGAAACAGTTTATTTGCCATT 600
539 ATCAATCGGATTTTATCGGCGTGCAGCTTGGCGCGCGGTGAAACAGTTTATTTGCCATT 598
601 GGTGCGGGGATGTCGACGGTATCGGTTTGGTTCGGAATGCGGTACGGCGCTGATCAC 660
599 GCGCGGGGATGTCGACGGATCGGCTTGGCGCGAAGCGCCGACGCGCTAATCACG 658
661 CGTGGCTGCGTGAATGTGCGTCTGTGTGCGCGCTGGGTGCGGACCTTGCACCTTT 720
659 CGTGGACTGACCGAAATGTGCGGCTTTGGCGC-ACGCTTGGCGCGGATCCCGCACCTTT 717
721 ATGGGCGATGCGGGGCTTGGGATCTGCTGTACCTGTACCGAAGAACCGTGCCTAAC 780
718 ATGGGATGCGGGTTTAGGCGATCTGTGCTGACCTGTACCGAAGAACCGTGCCTAAC 777
781 CGCGTTTTCGATGATGCTCGGTGAGGCGATGATGATCAAGCGCGCGAGGAAGATT 840
778 CGTGGTTTTCGATGATGCTTGGCGGCGATGATGATGATGATGATGATGATGATGAT 837
841 GGTGAGTGTGAGGCTACCGCAATACGAAGAGTCCGCACTGCGGCGATCGCTTC 900
838 GGCAGGTGTGAGGCTATCGCAATACGAAGAGTTCGTGAATTTGGCGCACCGTTT 897
901 GGCCTTGAATGCAATACCGAGGAATTTATCAAGTATTATTCGGAAGAACCGCG 960
898 GGTGTTGAATGCCAATACCGAGGAATTTATCAAGTATTATTCGGAAGAACCGCG 957
961 CGCGAGGAGCATTTGACTTTACTAGGTCTGTGACGCAAGGACGAGCGAGCCACTA 1019
958 CGCGAGGAGCATTTAAGTTTATAGGTGCGCGCGCAAGGAGGCTGAGTTCGCCACTA 1016

RESULT 10
ACA54019
ID ACA54019 standard; DNA; 1020 BP.
XX
AC ACA54019;

XX 19-JUN-2003 (first entry)
XX Prokaryotic essential gene #35676.
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX Yersinia pestis.
XX WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US0009107.
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948593.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JB, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
PR P-PSDB; ABUS0149.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 14; SEQ ID NO 41889; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are;
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 1020 BP; 238 A; 238 C; 288 G; 256 T; 0 U; 0 Other;

Query Match 59.4%; Score 606; DB 8; Length 1020;
Best Local Similarity 74.9%; Pred. No. 9.5e-179;
Matches 759; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

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OY 1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTCCGGCTCGTACGGCACGGCTCTT 60
DB |||||
OY 1 ATGAACCAACACCTGCTTCAATGCTGTATCGGTGCGGATCTTACGGCACCGCATTA 60
DB |||||
OY 61 GCCATCACCTGGCAAGAAATGGCCACAGAGTTGCTCTGGGGCCATGACCCCTGAACAT 120
DB |||||
OY 61 GCTATCACACTGGCGCGTAATGGCCATCAAGTCGTGTTATGGGGCCATGACCCCTAAACAT 120
DB |||||
OY 121 ATCGCAACGCTTGACCGGACCGCTGTAACCGCGTTTCTCCCGATGTCCTTTCC 180
DB |||||
OY 121 ATTCAACAGCTGCAACAAGACCGCTGTAAACCGCGCTTCTCCTACCTGATGCTCTTCC 180
DB |||||
OY 181 GATACGCTCCATCTTTGAAAGGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATCTC 240
DB |||||
OY 181 GATAGTTGCGATTGGAACCGACTTAGCATCTGCTGGCTGCGCAGCGGATGTGTG 240
DB |||||
OY 241 GTCGTGTAACCCAGCATGTCTTTGGTGAAGTGTGCGCCAGATTAACCACTGATGCGT 300
DB |||||
OY 241 GTCGTGTCGCCAGCATGTCTTTGGTGTGTTTACATCAGTTGAGCCCTCATCTACGT 300
DB |||||
OY 301 CCTGATGCGCTCTGCTGGCGACCAAGCGCTGGAAGCGGAACCGGAGCTCTGTTA 360
DB |||||
OY 301 AAGATGACGATGCTGTGGCAACCAAGGCTAGAAAGCTGAACCCGCGCTCTGCTA 360
DB |||||
OY 361 CAGGACGTGGCGGTGAGGCCCTTAGCGCATCAAAATTCGCTGGCGGTTATCTCTGGCCCA 420
DB |||||
OY 361 CAGGATGTGGCCGCGAAGTCTTGGCGAGGCTATCCGCTTGGCGTATCTTGGTCCA 420
DB |||||
OY 421 ACGTTTGCAGAAAGCTGGCGGAGTTTACGACAGCTATTTGCTGGCTCGACCGAT 480
DB |||||
OY 421 ACGTTTGCAGAAAGTGGCGGAGTTTACGACAGCTATTTGCTGGCGATTTGCTGGCATCGACCGAT 480
DB |||||
OY 481 CAGACCTTGGCGATGATCTCAGCAGCTGCTGCACTGGCGGCAAAAGTTTCGGTTTAC 540
DB |||||
OY 481 GTGCAATTTAGCGAAGATCTGCAACAGTTATTTGCACTGTGAAAAGCTTTGCGAGTTTAC 540
DB |||||
OY 541 AGCAATCCGATTTTCAATGGCGTGAGCTTGGCGCGGCTGMAAAAGTTTATTTGCCATT 600
DB |||||
OY 541 AGTAATCTGATTTTATCGGGGTACAGCTTGGTGGCGGAGTGAAGAAAGTATTTGCCATC 600
DB |||||
OY 601 GGTGGGGATGTCCGAGCTATCGTTTGGTGGCAATGCGCGTACGCGCTGATCACC 660
DB |||||
OY 601 GGTGCAAGTATGTCGATGCGATCGTTTGGTGGCAATGCGCGTACGCGCTCTAATAACC 660
DB |||||
OY 661 CGTGGCTGCGTGAATGCTGCTTGGTGGCGCTGGTGGCGACCTGCGACCTT 720
DB |||||
OY 661 CGCGGTTAGCGGAGATGACGCGCTTAGGGAGCGGATTTAGGTGGCGATCTTCCACCTTT 720
DB |||||
OY 721 ATGGGATGGCGGGCTTTGGCGATCTGCTGCTTACCTGTACCGAAACAGTTCGGTAAAC 780
DB |||||
OY 721 ATGGGATGGCAGGTTAGGCGATTTGGTGTAACTTCAAGATCAAGATCAATCCGCTAAC 780
DB |||||
OY 781 CGCGGTTTGGCATGATGCTCGTTCAGGGCATGATGTACAAAGCGCGCAGGAGAGATT 840
DB |||||
OY 781 CGCGGTTTGGCATGATGCTCGTTCAGGGCATGATGTACAAAGCGCGCAGGAGAGATT 840
DB |||||
OY 841 GGTGAGTGGTGGAGGCTACCGCAATACGAAGAGTCCGCAACTGGCGCATGCTCTTC 900
DB |||||
OY 841 GGTCAAGTGGTAGAAGGTTACCGTAATACCAAGGAAGTCTTGGCATTTAGCAGCGCTCAT 900
DB |||||
OY 901 GCGGTTGAAATGCCAATACCGAGGAATTTATCAAGTATTATTTGCGGAAAGAAACCG 960
DB |||||
OY 901 GCGGTCGAATGCCAATACCGAGGAATTTATCAAGTATTATTTGCTAAGATGCT 960
DB |||||
OY 961 CCGGAGGAGCATGATGCTTACTAGTCTGTCAGCAAGGAGCGAGCGCAGCAGC 1014
DB |||||
OY 961 CCGGAGGAGCATGATGCTTACTAGTCTGTCAGCAAGGAGCGAGCGCAGCAGC 1014
DB |||||
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RESULT 11
ABQ21987/c
ID ABQ21987 standard; DNA; 781 BP.

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XX ABQ21987;  
XX AC  
XX 12-JUL-2002 (first entry)  
XX  
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 8578.  
XX  
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
XX drug; side effect; cancer; central nervous system; cardiovascular;  
XX gastrointestinal; respiratory system; single nucleotide polymorphism;  
XX SNP; cell differentiation; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200218632-A2.  
XX  
XX 07-MAR-2002.  
XX  
XX 01-SEP-2001; 2001WO-EP010074.  
XX  
XX 01-SEP-2000; 2000DE-01043826.  
XX  
XX 05-SEP-2000; 2000DE-01044543.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
XX WPI; 2002-371829/40.  
XX  
XX Determining the degree of cytosine methylation in genomic DNA, useful for  
XX diagnosis and prognosis, comprises selective hybridization of amplicons  
XX from chemically treated DNA.  
XX  
XX Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
XX genomic sample of DNA. The sample is treated chemically to convert  
XX cytosine (C) but not methylated C, to uracil, then part of the genomic  
XX DNA that contains the target C is amplified to form a labeled amplicon.  
XX The amplicon is hybridised to two classes, each with at least one member,  
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
XX degree of hybridisation to both classes is determined from the label on  
XX the amplicon. From the ratio of labels hybridised to the two classes of  
XX oligomers, the degree of methylation is calculated. The method is used:  
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
XX and of a wide range of diseases, e.g. cancer, disorders of the central  
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
XX particularly by detecting mutations or single nucleotide polymorphisms  
XX (SNP's); and (ii) for differentiation of cell or tissue types and for  
XX investigating cell differentiation. The method allows the methylation  
XX status of many C residues to be determined simultaneously. ABQ1410-  
XX ABQ54121 represent genomic DNA sequences used to illustrate the method  
XX for determining the degree of cytosine methylation described in the  
XX disclosure of the invention  
XX  
XX Sequence 781 BP; 313 A; 239 C; 76 G; 153 T; 0 U; 0 Other;  
XX  
XX Query Match 55.5%; Score 565.6; DB 6; Length 781;  
XX Best Local Similarity 82.8%; Pred. No. 3.7e-166;  
XX Matches 646; Conservative 0; Mismatches 134; Indels 0; Gaps 0;  
OY 153 CGCGTTTCTCCCGATGCGCTTTTCCCGATGCGCTCCATCTTGAAGCGATCTCGCCAC 212  
DB |||||  
OY 780 CGCGTTTCTTTCGATGCTTTTATTTCGATGCGCTTTTATTTCGATGCTTTTTCGTTAT 721  
DB |||||  
OY 213 TGGCGTGGCAGCCAGCGCGTAATATCTCGTCTGTACCCAGCCATGCTTTTGGTGAAGT 272  
DB |||||  
OY 720 TGGCGTGGTGTAGTGTGTAATATTTTCGCTGTCTATTTATTTTGGTGAAGT 661  
DB |||||  
OY 273 GCTGGCGCAGATTAAACCACTGATGCGCTCTGATGCGCGTCTGGTGGGCGACCAAGG 332  
DB |||||  
OY 660 GTTGGCTTAGATTAAATTTATTTGATGCGGTTTTCGATGCGGTTTGGTGGCGGATTAAGG 601  
DB |||||
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Qy	333	GCTGGAACCGGAAACCGGACGCTCTGTTACAGACGCTGGCGCTGAGGCCCTTAGGCGCATCA	392
Db	600	GTTTGAACCGGAAATCGGACGTTTGTATAGACGTGGCGCTGATGATGTTTTTAGGCGCATTA	541
Qy	393	AAATTCGGCTGGCGGTATCTCTGGCCCAACGTTTCGGAAGAACCTCGGCGCAGGTTTACC	452
Db	540	AAATTCGTTGGCGGTATATTTTGGTTTAACTGTTTCGGAAGAATTTGGCGGTAGGTTTATC	481
Qy	453	GACAGCTATTTTCGCTGGGCTCGACCGGATCAGACCTTTGCGATGATCTCCAGCAGCTGCT	512
Db	480	GATAGTTATTTTCGTTGGTTTCGATCGATTAGATTTTTTGTGCAATGATTTTTTAGTAGTTGTT	421
Qy	513	GCACCTGGCGGCAAAAGTTTCCGCGTTTACAGCAATCCGGAATTTCAATGGCGGTGCAGCTGG	572
Db	420	GTAATTCGGGTAAAGTTTTCGCGTTTATAGTAATTCGGATTTTATTTGGCGTGTAGTTGG	361
Qy	573	CGGCGCGGTGAAAAACGTTTATGCCATTATGGTCGGGGATGTCGCACGGTATCGGTTTTGG	632
Db	360	CGGCGCGGTGAAAAACGTTATGTTTATTTGGTTCGGGGATGTTTCGACCGGTATCGGTTTTGG	301
Qy	633	TGCGAATCGCGGTACGGCGCTGATCACCGTGGGCTGGCTGAAATGTCGCGTCTGGTGC	692
Db	300	TGCGAATCGCGGTACGGCGTGTGATTTATTCGTGGGTGGTTGAAATGTCCGCTTTTGGTGC	241
Qy	693	GGCGCTGGGTCCGACCTCGCACCTTTATGGGCATGGCGGGCTTGGCGATCTGCTGCT	752
Db	240	GGCGTGGGTGTGATTTTGTATTTTTATGGGTATGGCGGGTTTGGCGATTTGCTGTT	181
Qy	753	TACCTGTACCGAAACACAGTCGCGTAACCGCCGTTTTGGCATGATGCTCGGTACAGGCAT	812
Db	180	TATTTGTATCGATAATTAGTCGCGTAATCGTTCGTTTTGGTATGATGTTTCGGTTAGGGTAT	121
Qy	813	GGATGTACAAACGCGCAGGAGAAGATTGGTCAGTGTGGAGGCTACCCGCAATACGAA	872
Db	120	GGAATGTATAAACGCGGTAGGAGAGATTGGTTAGGTGGTGGAAAGGTTATCGTAAATACGAA	61
Qy	873	AGAAGTCCGCGAATCGGCGGCATCGCTTCGGCGTTGAAATGCCAATAACCGAGGAATTTTA	932
Db	60	AGAAGTTCGCGAATGGCGGTATCGTTTCGGCGTTGAAATGTTTAATTCGAGCGAAATTTTA	1

XX

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ34121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.

Sequence 781 BP: 153 A; 76 C; 239 G; 313 T; 0 U; 0 Other;

Query Match 55.5%; Score 565.6; DB 6; Length 781;

Best Local Similarity 82.8%; Pred. No. 3.7e-166;

Matches	646;	Conservative	0;	Mismatches	134;	Indels	0;	Gaps	0;
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QY 153 CGCGTTTCTCCCCGATGTGCCCTTTTCCCGATAAGCTCCATCTTGAAAGCGATCTCGCCAC 212

Db 2 CGCGTTTTCGATGTTTATTCGATACGTTTATTTGAAAGTAAATTCGTTAT 61

QY 213 TGGCTGGCAGCCAGCCGTAATATTCTCGTCGTACCCAGCCATGCTTTTGGTGAAGT 272

62 TCGGTTGGTAGTTAGTCGTAATTTTCGTCGCGTATTAGTTATGTTTGGTGAAGT 121

QY 273 GCTGCGCCAGATTAAACCACTGATGCGTCCTGATGCGGCTCTGGTGTGGCGACCAAGG 332

D_b 122 GTGCGTTAGATTAAATTATTGATGCGCTTTTGATGCGCGTTTGGTGTGGCGATTAAAGG 181

333 GCTGGAAGCGGAAACCGGACGTCTGTACAGGACGTGGCGCGTGAGGCCTTAGGCGATCA 392

D_b 182 GTTGGAGCCGAAATCCGACGTTTGTTATAGCACGTGGCGCGTGATGTTTACGCCGATTA 241

393 AATTCCGCTGCGGGTTATCTCTGCCCCAA CGTTTGCGAAAGAACTGGCGGCAGGTTTACC 452

242 AATTTCGTTGGCGGTATATTTTGGTTAACGTTTGGCGAAAGAAATTGGCGGTAGGTTTATC 301

OV 453 GACAGCTATTTCGGCTGGCGCTCGACCGATCAGACCTTTGCCGATGATCTCCAGCAGCTGCT 512

302 GATAGTTATTCTGGTTTCGATTCGATTGTTGTCGATGATTTTGTAGTGGT 361

513 GCACTGGGCAAAAGTTTCCGGTTTACAGCAATCCGGATTTCATTGGCGTGCAGCTTGG 572

362 GTATTGGCTAAAGCTTTTCGGCTTATAGTAA TTCCGATTTTATTGGCGTGTAGTTGG 421

573 CGGCGCGGTGAAAAACGTTATTGCCATTGGTCCGGGGA TGTCGACGGTATCGGTTWTGG 632

423 CCGCCGCTGAAAGCCCTATTCCTATTCCTGCGCGGATGTTTCAAGGTTTGG 481

633 TCCGAAATGGCGCTACCGCGCTGATCAACCGTGGGTGAAATGTCCGCTCTTGGTGC 692

483
541

603 CCCCCCTCCGCGCCGCTTATCGGCATGGCGGGCGTTGGCGATCTGGTGGT 752

601

Db 968 CTCAGGCATTATTAGGAAGACCAGAAAGGATGAGAC 1005

RESULT 14
ACF65374

ID ACF65374 standard; DNA; 69727 BP.

XX ACF65374;

XX 20-NOV-2003 (first entry)

XX Photorhabdus luminescens nucleotide sequence #27.

XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.

XX Photorhabdus luminescens.

XX WO200294867-A2.

XX 28-NOV-2002.

XX 07-FEB-2002; 2002WO-IB003040.

XX 07-FEB-2001; 2001FR-00001659.

XX (INSP) INST PASTEUR.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;

XX WPI; 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX Claim 1; SEQ ID NO 27; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes

XX SQ Sequence 69727 BP; 20213 A; 13239 C; 14632 G; 21638 T; 0 U; 5 Other;

Query Match 54.5%; Score 556.4; DB 10; Length 69727;
Best Local Similarity 72.3%; Pred. No. 2.5e-162;
Matches 722; Conservative 0; Mismatches 276; Indels 0; Gaps 0;
Qy 11 GTAAATGCTTCAATGACTGTGATCGGTCGGCTCGTACGGCACCGCTTTGCCATACCC 70
D5 54182 GTACTGTTCTTATGACAGTGTATGTCGGCTCATACGGCACCTATTAGCCATTACGC 54241

Qy 71 TGGCAAGAAATGGCCACGAGGTTGCTCTCTGGGGCCATGACCTGAACATATCGCAACGC 130
Db 54242 TGGCTCGTAATGGTCAATAATGTTGTACTTTTGGGGGCATAATCCAGAGCATGTTGGGGCAT 54301
Qy 131 TTGAACCGCACCGCTGTAAACGCGCGTTCTCCCGCATGTGCCCTTTTCCCGATACGCTCC 190
Db 54302 TGCNAACGGGTGCGTTGTAATCAAAAATTTCTGCGGATGTTCTCTTCTCGATAGTTAT 54361
Qy 191 ATCTTGAAGCGATCTCGCCACTGCGCTGGCAGCCAGCGTAATATTTCTCGTCTCGTAC 250
Db 54362 TGCTTGAACCGACCTAATAAAGCACTAAACAGCGAGCGCGATATTTCTTGTGTGGTAC 54421
Qy 251 CCAGCATGCTTTGGTGAAGTCTGCGCCAGATTAACACCTGATCGCTCTCATCGC 310
Db 54422 CTAGCCATGTTTGGTGAAGTGTAAAGCAGATAAAACACATTTACGGCTCATTCAC 54481
Qy 311 GTCTGTGTGGGCGACCAAGGGCTGGAAGCGGAACCGGACGCTCTGTACAGACGCTGG 370
Db 54482 GTATCGTATGGGCAACTAAGGCTTGGAGCGGATACCGTGGTATTCAGGATGTGG 54541
Qy 371 CGCGTAGGCTTAGGCGATCAAAATCCGCTGGCGGTTATCTCTGGCCCAACGTTTGGCA 430
Db 54542 CCGCTGAGATATTAGGCAATGAATACCGCTAGCGGTGCTCTCTGGGCGCAACATTTGCTA 54601
Qy 431 AAGNACTGGCGGCGAGGTTTACCGACAGCTATTTCCGCTGGGCTCGACCGATCAGACCTTG 490
Db 54602 AAGAGTTAGCGGCTGGTTTGCCTACCGCGATGCTATTTCCGCGACGGAATCTCTTTTG 54661
Qy 491 CCGATGATCTCCAGCAGCTGCTGCACCTGCGCGCAAAAGTTTCCGCGTTTACAGCAATCCGG 550
Db 54662 GCGATGACTTCAACATATTCCACTGTGCAAAAGTTTCCGCGTTTATAAATCCTG 54721
Qy 551 ATTTCAATGGCGTGCAGCTTGGCGGCGGCTGAAAAAGTTATTTGCTGTCGCGGGA 610
Db 54722 ATTTTATGTTGTTCAACTCGGTGGTGGTGTAAAAACGCTGATCGCCATTGGCGCGGAA 54781
Qy 611 TGCCGACGCTACCGGTTTGGTGGCAATCGGCTACGGCGCTGATCACCGTGGGCTGG 670
Db 54782 TATCTGATGGCATGGGATTTGGTGTAAATGCTGACCGCATGATTTACTCGTGATGG 54841
Qy 671 CTGAAATGTCGCGTCTTTGGTGGCGGCTGGGTGCGGACCTGCCACCTTTATGGGCATGG 730
Db 54842 CGGAATGAGTCGCTTGGTGCAGCGCTTGGTGTGATCTCTACCTTTATGGGCATGG 54901
Qy 731 CGGGGCTTGGCGATCTGGTGCCTTACCTGTACCGAAAAACAGTCCGCTAACCGCGTTTG 790
Db 54902 CGGGATTTGGGCGATTTGGTCTTAACTTGTACTGATAACCAATCACGTAACCGCTGTTG 54961
Qy 791 GCATGATGCTCGGTTCAGGCGCATGATGTACAAAGCGCGCAGGAGAGATTGGTCAGGTGG 850
Db 54962 GCATGATGCTGGGCGAGGAAATCAGTGTGAAGAGCGCGAGTATCAGATTGGGCGAGTTG 55021
Qy 851 TGAAGGCTTACCGCAATACGAAAGAAAGTCCGCGCAATCGGCGCATCGCTTGGCGCTTGA 910
Db 55022 TTGAAGTATTCGCAATACCAAGAAAGTACGTGCTGCTTAATCGGCCAATGTAGAAA 55081
Qy 911 TGCCAAATACCGAGGAAATTTATCAAGTATTATTTCCGGAATAAAACCGCGCGAGGAG 970
Db 55082 TGCCGATTTGAGAACAAATCTACCGATATCTTATTCGAATAAAATGTGATAGAAGCTG 55141
Qy 971 CATTTGACTTTACTAGGTCGTGACGCAAGGACGAGCGC 1008
Db 55142 CTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAGAC 55179

RESULT 15

ACF67367 35

Continuation (36 of 57) of ACF67367 from base 3500001 (Photorhabdus luminescens nucleotide sequence 3500001-3500001)

WP Sequence split into 57 fragments

WP Fragment Name

WP ACF67367_00

WP ACF67367_01

WP ACF67367_02

WP ACF67367_03

WP ACF67367_04

WP ACF67367_05

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WP ACF67367

WP	ACF67367_03	300001	410000
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WP	ACF67367_55	5500001	5610000
WP	ACF67367_56	5600001	5648894

Query Match

Best Local Similarity

Matches 722; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

Qy	11	GTAAATGCTTCAATGACTGTGATCGGTGCGCGCTGTACGGCACCGCTCTTGCCATCACCC	70
Db	79833	GTACTGTTTCTATGACAGTATGTTGGCGCGCTCATACGGCACCTCATTAGCCATTACGC	79892
Qy	71	TGGCAAGAATGGCCACAGGTGTCTCTGGGGCATGACCTTGAAACATATCGCAAGC	130
Db	79893	TGGCTGCTAAATGGTCTAATGTTGTAATTTGGGGGCATTAATCCAGAGCATGTGGGGCAT	79952
Qy	131	TGAAACGGCAGCGCTGTAAACGCCGGTCTTCCCGATGTGCTTTCCCGATACGCTCC	190
Db	79953	TGCAACGGGTGGTGTGTAATCAAAATTTTGGCGGATGTTCTTCTTCTGATAGTTAT	80012
Qy	191	ATCTTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCGTAATATTTCTCGTCTGCTAC	250

Db	80013	TGCTTGAACCGGACCTAATAAAGCACTAACACAGCGAGCCGGATATTTCTGTTGGTAC	80072
Qy	251	CCAGCCATGCTTTGGTCAAGTGTGCGCCAGATTTAAACCACTGATCGTCTGTATGGC	310
Db	80073	CTAGCCATGTTTGGTGAAGTGTAAAGCAGATAAAACCCACATTTACGGCTGATCAC	80132
Qy	311	GTCTGGTGTGGCGACCAAAAGGGCTTGAAGCGGAAACCGGACGTCGTGTTACAGGACGTGG	370
Db	80133	GTATCGTATGGGCAACTAAAGGCTTGGNAGCGGATACGGTCCGTTATTGCGAGATGG	80192
Qy	371	CGCTGAGGCTTATAGGCGATCAAAATTCGCTGGCGGTTATCTCTGGCCCAACGTTTGGGA	430
Db	80193	CCCGTGAGATATTAGGCAATGAAATACCGCTAGCGGTGCTCTCTGGGCAACATTTGCTA	80252
Qy	431	AAGAACTGGCGCAGGTTTACCGACAGCTATTTTCGCTGGCCTCGACCGATCAGACCTTTG	490
Db	80253	AAGAGTTAGCGCGTGGTTCCTACCGGATGCTATTTCCGCGACGGAAATCTGCTTTTG	80312
Qy	491	CCGATGATCTCCAGCAGCTGCTGCACCTCGCGCAAAAGTTTCCGGGTTTACAGCAATCCGG	550
Db	80313	CGGATGGACTTCAACAATTTATCCACTGTGGCAAAAGTTTCCGGGTTTATAAAATCTG	80372
Qy	551	ATTTCAATTGGCGTGACGCTTGGCGCGGCGTGA AAAAGTTATTGCCATTTGGTGGCGGA	610
Db	80373	ATTTTATTTGGTGTTCAACTCGGTGTCGCGTAA AAAACGTCATGCCATTTGGCGGGAA	80432
Qy	611	TGTCGACGGTATCGGTTTTGGTGGCAATGCGCTACGGCGCTGATCACCGTGGGCTGG	670
Db	80433	TATCTGATGGCATGGGATTTGGTGTAA TGTCTGCTACCGCATTGATTA TCTCGTGATTTG	80492
Qy	671	CTGAAATGTCGCTCTTTGGTGGCGGCTGGGTGCGGACCTTGCCACCTTTTATGGGCATGG	730
Db	80493	CGGAAATGAGTCGCTTGGTGGCGGCTTGGTGTGCTGATCTTCTTACCTTTTATGGGCATGG	80552
Qy	731	CGGGCTTGGCGATCTGGTGTCTTACCTGTACGAAAACAGTCGCGTAACCGCGCTTTTG	790
Db	80553	CGGGATTTGGCGATTTGGTCTTAACTTTGTA CTGATAACCAATCACGTAACCGTCTGTTTG	80612
Qy	791	GCATGATGCTCGGTCAGGGCATGATGTACAAAGCGCGCAGAGAGATTGGTCAGGTGG	850
Db	80613	GCATGATGCTGGGCGCAGGGAATCAGTGTGAAGAGCGCAGTATCAGATTGGGCAGGTG	80672
Qy	851	TGGAAGGCTACCGCAATACGAAAGAGTCCCGCAACTGGCGCATCGCTTCGCGCGTTGAAA	910
Db	80673	TTGAAGGTTATCGCAATACCAAGAGTACGTGCTATGGCTAATCGGCCAATGTAGAAA	80732
Qy	911	TGCCAATAACCGAGGAAATTTATCAAGTATTTATTTGGGGA AAAAACCGCGCGGAGGAG	970
Db	80733	TGCCGATTTGCAGAA CAAATCTACCAAGATCTCTATTGCAATAAAAATGTGATAGAAGCTG	80792
Qy	971	CATTGACTTTTACTAGGTCTGTCACGCAAGGACGAGCGC	1008
Db	80793	CTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAGAGC	80830

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